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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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           GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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US-07-885-089B-35

US-07-885-089B-2

US-07-885-089B-8

US-07-885-089B-6

US-07-885-089B-6

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Sequence 7, Appli Sequence 228, App Sequence 228, App Sequence 11381, A Sequence 35, Appli Sequence 9, Appli Sequence 9, Appli Sequence 6, Appli Sequence 10, Appli Sequence 10, Appli Sequence 4, Appli Sequence 9, Appli Sequence 34, Appli Sequence 34, Appli Sequence 37, Appli Sequence 17, Appli Seq
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Query Match Best Local Similarity Matches 252; Conservat	US-07-885-089B-7 US-07-885-089B-7 i Sequence 7, Application US/07885089 patent No. 5830995 i GENERAL INFORMATION: APPLICANT: Shoyab, Mohammed APPLICANT: McDonald, Vicki L. APPLICANT: WcDonald, Vicki L. APPLICANT: Bradley, James G. APPLICANT: PLOWMAIN, Gregory D. TITLE OF INVENTION: HEPARIN-BIN INTITLE OF INVENTION: STREET INFORMATION: INTITLE OF SECURAL INFORMATION: INTITLE OF SECURITY INFORMATION: INTELEPHONE: 212-790-909 INTELEPHONE: 212-790-909 INTELEPHONE: 212-869-9741 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 252 amino acidd INFORMATION SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: INFORMATION SEQ ID NO: 7: SEQUENCE SEQUENCE SEQ ID NO: 7: SEQUENCE TYPE: MINIO SEQUENCE	28 454 34.7 30 454 34.7 31 454 34.7 32 454 34.7 33 454 33.8 356 440 33.8 356 433 33.1 39 47.5 26.6 40 320 24.5 45 320 24.5 320 24.5 320 24.5 320 24.5 320 24.5 320 24.5
100.0%; Score 1308; DB 2; Lengt: 100.0%; Pred. No. 8.2e-122; 1ve 0; Mismatches 0; Indel	B INS: A FAMILY OF IDING EPITHELIAL CELL LP Hericas 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.0	87 2 US-08-330-161-15 87 2 US-08-440-401-15 87 2 US-08-440-401-15 87 2 US-08-419-878B-15 87 3 US-09-173-480-15 87 5 PCT-US92-04295A-17 87 5 PCT-US92-04295A-17 87 2 US-07-885-089B-33 95 2 US-07-885-089B-31 97 2 US-07-885-089B-32 98 2 US-07-885-089B-32 99 2 US-07-885-089B-31 10 US-08-487-743B-18 87 1 US-08-456-241-18 87 2 US-08-456-241-18 87 2 US-08-440-401-16 87 2 US-08-440-401-16 87 2 US-08-410-878B-16
ngth 252; dels 0; Gaps 0;	GROWTH FACTORS	Sequence 15, Appl Sequence 17, Appl Sequence 15, Appl Sequence 15, Appl Sequence 17, Appl Sequence 18, Appl Sequence 33, Appl Sequence 31, Appl Sequence 30, Appl Sequence 31, Appl Sequence 31, Appl Sequence 11, Appl Sequence 16, Appl

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RESULT 3
US-09-919-039-228
, Sequence 228, Application US/09919039
, Patent No. 6727066
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ITITE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
CURRENT APPLICATION GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
CURRENT APPLICATION NUMBER: US/09/976,594
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
SOFTWARE: PERL PROGRAM
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAMES/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 3478236CD1
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Best Local Similarity
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US-09-976-594-582
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Patent No. 66
                                                                                                                                                                                                                   241 LRQENGNVHAIA 252
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6673549
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                                                                                                                                       APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 05/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PR
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FILE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES

CURRENT APPLICATION NUMBER: US/09/919,039

FRICK FILING DATE: 2002-09-09

PRIOR PELLING DATE: 2000-07-28

SOFTWARE: PELL PROS: 401

SEQ ID NO 228

LENGTH: 252

TYPE: PRT

ORGANISM: Homo Bapiens
FEATURE:
NAMES/KEY: misc feature
US-09-919-039-228

US-09-919-039-228
                                                                                                             i ORGANISM: Human
US-09-949-016-11381
Query Match

100.0%; Score 1308; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.2e-121;
Matches 252; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11381, Applicat:
Sequence 11381, Applicat:
Patent No. 6812339
GENERAL INFORMATION:
CANT: VENTER, J. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-949-016-11381
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Best Local Similarity
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Pred. No. 8.2e-122;
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METHODS OF DETECTION AND USES THEREOF
                                     Length 322;
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Matches

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US-07-885-089B-35
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                                                                                                                                       US-07-885-089B-35
                                                                 Query Match
Best Local S
Matches 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35, Application US/07885089B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: McDonald, Vicki L.
APPLICANT: Bradley, James G.
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: AMPHIREGULINS: A FAMILY OF
TITLE OF INVENTION: HEPARIN-BINDING EPITHELIAL CELL GROWTH FACTORS
                                                                                                                                                                                                                                       TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: COTUZZÍ, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5624
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,089B
FILING DATE: 18-MAY-1992
                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1155 AV
CITY: New York
STATE: New York
COUNTRY: USA
                                                    Local 226,
                                                                                                                                                                                                                                                                             TELEPHONE: 212-19741
                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 18
CLASSIFICATION:
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                                                                                                                                                                                                                      ENGTH:
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                                                                                 Similarity
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                                LDLNDTYSGKREPFSGDHSADGFEVTSRSEMSSGSEISPVSEMPSSSEPSSGADYDYSEE 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
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1155 Avenue of the Americas
                                                                                                                                                                                                                      226 amino acids
                                                                                                                                                                       unknown
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                                                                                                                                                     protein
                                                                                                                                                                                      single
                                                               90.0%; Score 1177; DB 2;
100.0%; Pred. No. 7.3e-109;
tive 0; Mismatches 0;
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                                                                                                 Length 226;
                                                                  Indels
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US-08-208-008C-9
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                                                                                                                                                                                  Matches
                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION UNMER: 33,073
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-I
SOFTWARE: WORD PERFECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MEISSNER, ET AL.
TITLE OF INVENTION: Transformin
TITLE OF INVENTION: Alpha - H1
                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
LENGTH: 192 AMINO ACI
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STREET: 6 L.
CITY: ROSELAND
CTATE: NEW JERSEY
"ISA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA,
                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
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TOPOLOGY: LI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/
FILING DATE: March 8, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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121 SDKPKRKKKGGKNGKNRRNRKKKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGER
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                                                                                                                                                                                                                                                                                                               AMINO ACID
                                                  SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENT
                                                                        SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENT
                                                                                                                 MRAPLLPAAPVVLSLLILGSGHYAAGLDLN-TYSGKREPFSGDHSADGFEVTSRSEMSSG
                                                                                                                                                MRAPLLPPAPVVLSLLILGSGHYAAGLDLNDTYSGKREPFSGDHSADGFEVTSRSEMSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGERCGEKSMKTHSMIDSSLSKIALAAIAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENTSDKPKRKKKGGKNGKNRRNRKKKNPC
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E: CECCHI, STEWART
6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                192 AMINO ACIDS
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                  LINEAR
                                                                                                                                                                                                                                                                PROTEIN
                                                                                                                                                                                               77.68;
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                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                               Score 1015.5; DB 1; Pred. No. 6.5e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                               325800-98
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                                                                                                                                                                                  0;
                                                                                                                                                                                  Indels
                                                                                                                                                                                                                Length
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                                                                                                                                                                                Gaps
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TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
                                                                                                                                                                                                                                                                   Query Match 76.8%;
Best Local Similarity 77.5%;
Matches 196; Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, 1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5830995
                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5624-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -07-885-089B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/OFFILING DATE: 18-MAY-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            TYPE: ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                         240
                                                   175
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                                                                             181
                                                                                                         115
                                                                                                                                    121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                 61
                                                                                                                                                                                           61
                                                                                                                                                                                                               KLRQENGNVHAIA 252
                              CGEKŚMKTQŚMVDŚDLŚKIALAAIAAFVŚAMTFTAIAVFITILLŔĸRCLĸĠŶĿĠVAĿĿĸĸ
                                                  CGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVAV-ITVOLRRQYVRKYEGEABERK 239
                                                                                                       SDKPKRKKKGGKNGKNRRNRKKKNPCNABFQNFCIHGECKYIEHLEAVTCKCQQEVFGER 180
                                                                                                                                         ŚETPĖGGĖL-----ŚSVIDYDYAĖEYDNĖPOISGYIVDDŚVRVEOVVXPKKNKTESEKT
                                                                                SDKPKRKKKGGKNGKNRKKKKKKKLCDTBFQNFCIHGKCTFLEQLETVSCQCYPBYFGBR 174
                                                                                                                                                             SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENT 120
                                                                                                                                                                                              MRA PLLEPPA PVVLSLLIPGSAHÝTAGLDVNÍDTÝSGKGEPPSGDHSADR PEVTSRSEISSA
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                                                                                                                                                                                                                                                                                                                                                                     amino acid
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1155 Avenue of the Americas
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Bradley, James G.
Plowman, Gregory D.
NVENTION: AMPHIREGULINS:
                                                                                                                                                                                                                                                                                                                                           protein
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HEPARIN-BINDING EPITHELIAL CELL GROWTH FACTORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/07/885,089B
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                                                                                                                                                                                                                                                          Score 1004.5; DB 2;
Pred. No. 1.2e-91;
9; Mismatches 31;
                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                    Length 247;
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TOPOLOGY: unkr
MOLECULE TYPE: I
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/885,089B
FILING DATE: 18-MAY-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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US-07-885-089B-8
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: COTUZZI, LAURA A. 742
REGESTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT: McDonald, Vicki L.
APPLICANT: McDonald, Vicki L.
APPLICANT: Bradley, James G.
APPLICANT: Plowman, Gregory D.
APPLICANT: AMPHREGULINS:
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                 240
                                                             175
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                                                                                                                  121 SDK¢KRKKKGGKNGKNRRNRKKKNÞCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGER 180
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                         KLROENGNVHAIA 252
                                       CGEKSMKŤQSMVĎSDĽŠŘÍÁĽÁÁĽÁÁFVSÁMTFŤÁĽÁVFÍŤILĽŘŘRCLŘGÝEGVÁŠEŘŘ
                                                      KLRQENGNAHAVA 247
                                                                                             SDKPKRKKKGGKNGKNRKKKKKKLCDTBFQNFCTHGKCTFLBQLETVSCQCYPBYFGBR
                                                                                                                                                  SETPPGGÉL-----SŚVIDYDYAEŻYDNEPQISGY I VDDŚVRVEQVVKPKKNKTESEKT
                                                                                                                                                                      SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYTVDDSVRVEQVVKPPQNKTESENT 120
                                                                                                                                                                                                       MRAPLIPPAPVVLSLLIPGSAHYTAGLDVNDTYSGKGEPFSGDHSADRPEVTSRSEISSA 60
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>. 5830995
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31;
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US-07-885-089B-10
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; Patent No. 5830995
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Best Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,089B
FILING DATE: 18-MAY-1992
CLASSIFICATION: 530
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acid
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NAME: CGLIZZI, LAULA A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 5624

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212,790-9090
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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ZIP: 10036
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                                                                                                                                  RKKLRQENGNVHAIA 252
                                                                                                                                                                                                        CGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVA---VITVQLRRQYVRKYEGEAEE 237
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                                                                                                                                                                                                                                                                                                                             REVSTISEMPSGSELSTG-DYDYSEEYDNEPQISGYIIDDSVRVEQVIKPKKNKTEGEKS
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                                                                                                                                                                                   CGEKSMKTHSEDDKDLSKIAVVAVTIFVSAIILAAIGIGIVITVHLWKRYFREYEGETEE
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AMPHIREGULINS:
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RESULT 11
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TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5624
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
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APPLICANT: McDonald, Vicki L.
APPLICANT: Bradley, James G.
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: AMPHIREGULINS:
TITLE OF INVENTION: HEPARIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
LENGTH: 248 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: sing TOPOLOGY: unknown
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CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                      234 RRRIRGENGTVHAIA 248
                                                                                                                                      174 CGEKSMKTHSEDDKDLSKIAVVAVTIFVSAIILAAIGIGIVITVHLMKRYFREYEGETEE
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                                                                                                                                                                                                         114 TEKPKRKKKGGKNGEGRRNKKKKNPCTAKFQNFCIHGECRYIENLEVVTCNCHQDYFGER
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                                                                                                                                                                                                                                                                             55 REVSTISEMPSGSELSTG-DYDYSEEYDNEPQISGYIIDDSVRVEQVIKPKKNKTEGEKS
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EPITHELIAL (
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Sequence 4, Application US/07885089B Patent No. 5830995

GENERAL INFORMATION:
APPLICANT: Shoyab
APPLICANT: McDona

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RESULT 12
US-07-885-089B-9
                                                GENERAL INFORMATION:
APPLICANT: Shoyab,
APPLICANT: McDonal,
APPLICANT: Bradley
APPLICANT: Plowman
                                                                                                                                    sequence 9, Application US/07885089B
                                                                                                                                                      Sequence
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APPLICANT: Shoyab, Mohammed
APPLICANT: McDonald, Vicki L.
APPLICANT: McDonald, Vicki L.
APPLICANT: Bradley, James G.
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: AMPHIREGULINS: A FAMILY OF
TITLE OF INVENTION: HEPARIN-BINDING EPITHELIAL CELL GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5624
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,790,9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 243 amino acids
TYPE; amino acid
TOPOLOGY; linear
MOLECULE TYPE; protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 18-MAY-1992
CTACCITCH MUMBER: US/07/885,089B
FILING DATE: 18-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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les 177; Conservative
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APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: AMPHIREGILINS: A FAMILY OF
TITLE OF INVENTION: HEBARIN-BINDING EPITHELIAL CELL GROWTH FACTORS
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ZIP: 10036
                                                                                                                                                                                                                          230 RRÍROENGTAHAÍA 243
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                 180
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MOLECULE TYPE:
US-07-885-089B-9
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Best Local Similarity
Matches 177; Conserv
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RESULT 13
5202428-2
;Patent No. 5202428
; APPLICANT: SCHUBERT, DAVID
; TITLE OF INVENTION: DNA ENCODING NEUROTROPHIC GROWTH FACTOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/590,359
FILING DATE: 27-SEP-1990
; PRICK APPLICATION DATA:
APPLICATION NUMBER: 541,276
FILING DATE: 20-JUN-1990
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
STRANDEDNESS: 8:--
MOLECTP-OGY: 8:--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 562.
TELECHMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 18-MAY-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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1155 Avenue of the Americas
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Pred. No. 9.3e-79;
!4; Mismatches 40;
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229

170 179

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RESULT 15
US-07-885-089B-34
; Sequence 34, Application US/07885089B
; Patent No. 5830995
; GENERAL INFORMATION:
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5202428-2
;Patent No.
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LENGTH: 243
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Best Local Similarity
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TITLE OF INVENTION: DNA ENCODING NEUROTROPHIC GROWTH FACTOR
NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/590,359
FILING DATE: 27-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 541,276
FILING DATE: 20-JUN-1990
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                                                                                                                                                                                           RCGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVAVIT-VQLRRQYVRKYEGEAEER 238
                                                                                                                                                                                                                                              SDKPKRKKKGGKNGKNRRNR-KKKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGE 179
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                                                                                                             RRIRGENGTAHAIA 243
                                                                                                                                       KKLRQENGNVHAIA 252
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                                                                                                                                                                                                                                                                                                                                                                                                        66.9%; Score 874.5; DB 6; 69.7%; Pred. No. 9.3e-79; vative 24; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.9%; Score 874.5; DB 6; 69.7%; Pred. No. 9.3e-79; tive 24; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                    Query Match
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885
FILING DATE: 18-MAY-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LBUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5624
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 158 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIF: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Shoyab, Mohammed
APPLICANT: McDonald, Vicki L.
APPLICANT: Bradley, James G.
APPLICANT: Bradley, James G.
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: AMPHIREGULINS: A FAMILY OF
TITLE OF INVENTION: HEPARIN-BINDING EPITHELIAL (
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                     / Match 65.4%; Score 855; DB 2; Lu
Local Similarity 100.0%; Pred. No. 4.4e-77;
les 158; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
121
                      147 NABFQNFCIHGECKYIEHLEAVTCKCQQEYFGERCGEK 184
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                                                                                                        YDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENTSDKPKRKKKGGKNGKNRRNRKKKNPC 146
                                                                                                                                                                                            LDLNDTYSGKREPFSGDHSADGFEVTSRSEMSSGSEISPVSEMPSSSEPSSGADYDYSEE
NAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGERCGEK
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0,
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		Human	Human	Human	Monkey	_				-	-	-			•	_	Bovin	Mouse		Human

ALIGNMENTS

ABR47391 standard; protein; 252 8

ABR47391;

12-JUN-2003 (first entry)

Breast cancer associated protein sequence SEQ ID NO:13

Human; breast cancer; cytostatic; gene therapy.

Homo sapiens.

WO2003004989-A2

16-JAN-2003.

21-JUN-2002; 2002WO-US019669

21-JUN-2001; 2001US-0299887P.
27-JUN-2001; 2001US-0301572P.
18-JUL-2001; 2001US-0306501P.
25-SEP-2001; 2001US-0305002P.
05-MAR-2002; 2002US-0362585P.
14-MAY-2002; 2002US-0380391P.

Result No.

(MILL-) MILLENIUM PHARM INC.

Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S; Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE; Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;

WPI; 2003-210381/20. N-PSDB; ACC50082.

Breast cancer diagnosis of a marker in a patient cancer sample. or treatment t sample with by comparing the level of expression that in the control non-breast

Claim 1; SEQ ID NO 13; 128pp; English.

The present invention describes a method for assessing whether a patient is afflicted with breast cancer. The method comprises comparing the level of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and ABR47386 to ABR47632) in a patient sample and the normal level of expression of the marker in a control non-breast cancer sample, where a significant increase in the level of expression of the marker in the

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The invention describes a which are differentially
                                                                              New cDNAs, which are differentially expressed in (metastatic) breast cancer useful for diagnosing or staging, breast cancer, or for monitoring the treatment of breast cancer in an individual.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Breast cancer; differential gene expression; BC-cDNA; breast cancer diagnosis; breast cancer monitoring; breast cancer treatment; breast cancer staging.
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                                                      SEQ ID NO 2; 30pp; English.
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A combination of cDNAs (designated BC-cDNAs), Y expressed in breast cancer. The combination

Composition comprising several cDNAs that

are differentially expressed

ij

WPI; 2004-031227/03. N-PSDB; ADE77062.

Kaser MR;

(KASE/) KASER M R.

28-JUL-2000; 2000US-0222113P. 30-JUL-2001; 2001US-00919039.

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RESULT 3
ADE77063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               includes 152 cDNA sequences, or their complements. The protein encoded by CC compounds to identify at least one ligand that specifically binds the protein, producing or preparing polyclonal or monoclonal antibodies, or cc bind the protein differentially expressed in breast cancer is useful for cc detecting the expression of a protein in a sample. The antibodies, which specifically cc useful for diagnosing, monitoring the treatment of, or staging, breast cancer is the amino acid sequence of a differentially expressed cc cancer. This is the amino acid sequence of a differentially breast cancer associated protein. Note: The squence data for this part of the printed specification, but was obtained in cc sequence format directly from the US patent office at
                                                                                                                                                               US2003108871-A1.
                                                                                                                                                                                     human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
                                                                                                                                         12-JUN-2003.
                                                                                                                                                                                                                                            Human protein expressed in a liver disorder #62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
                                                                                                                                                                                                                                                                       29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                      ADE77063;
                                                                                                                                                                                                                                                                                                                  ADE77063 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                             241 LRQENGNVHAIA 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1308;
100.0%; Pred. No. 2.;
Conservative 0; Mismatches
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2.2e-113;
98 0;
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for treating liver disorder such as hyperlipidaemia, hypertension, type CC II diabetes, tumours of the liver and disorders of the inflammatory and commune response. The composition is useful for a high-throughput method cC immune response. The composition is useful for a high-throughput method cC of screening several molecules or compounds to identify a ligand which cC in the cDNA is useful for a cC inflammatory and compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with cC several of molecules or compounds under conditions to allow specific binding, and detecting specific binding between the protein and cC molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and cC quantifying differential gene expression, can be used in gene therapy, to cformulate prognosis and to design a treatment regimen and to monitor the cefficacy of treatment. The present sequence represents the amino acid convergence of a protein encoded by a cDNA differentially expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 252
                                                                                                                                     tyrosine kinase activity; type 1 plasminogen activator inhibitor; PAI-1;.
TIMP-1; tissue inhibitor of metalloproteinase 1; vinculin;
                                                                                                                                                                                                                  11-MAR-2004
                                                                                                                                                                                                                                                                          ADH17052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treated human C3A liver cell cultures, useful for treating liver disorders.
                                                WO2003097854-A2
                                                                                                                       vascular endothelial
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                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVAVITVQLRRQYVRKYEGEAEERKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SØKPKRKKKGGKNGKNRRNRKKKNPCNABFQNFCIHGECKYIEHLEAVTCKCQQEYFGER 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SBISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENT 120
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                  protein.
                                                                                                                                                                                                               .entry)
                                                                                                       itor of metalloproteinase 1; vinculin; growth factor; VEGF; placental growth factor; MIG; human; amphiregulin.
                                                                                                                                                                                                                                                                                                                                                    252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a composition comprising several cDNAs in a liver disorder. The composition is
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Pred. No. 2.2e-113;
Mismatches 0;
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                                                                                                  placental growth amphiregulin.
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Hepatotropic; Gene therapy; Wilson disease; liver disorder;
                               Human steroid-induced C3A liver cell protein #92.
                                                             06-MAY-2004
                                                                                           ADL12853
                                                                                                                     ADL12853 standard; protein;
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(first

entry)

252

240

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120

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The invention relates to a novel method for determining whether a test compound inhibits tyrosine kinase activity in a mammal comprising measuring in the mammal the level of at least one of the proteins and/or manual transcripts or genes for such proteins comprising type 1 plasminoger activator inhibitor (PAI-1), TIMP-1 (tissue inhibitor of metalloproteinase 1), vinculin, vascular endothelial growth factor (WEGF), placental growth factor (PMF), VEGF/PLGF heterodimers or migration inhibitory factor (MMG), exposing the mammal to the test compound and then measuring in the mammal the level of at least one of the proteins and/or mRNA transcripts previously measured. The method of the invention may be useful for determining whether a test compound in this tyrosine kinase activity in a mammal. The current sequence is invention the tyrosine kinase activity inhibition-related protein of the
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining whether a test compound inhibits tyrosine kinase activity a mammal by exposing the mammal to the test compound and measuring in mammal the level of at least one of the measured proteins or mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2002; 2002US-0380872P
24-FEB-2003; 2003US-0448874P
24-FEB-2003; 2003US-0448922P
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morimoto A,
Walter SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAY-2003; 2003WO-US015711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcripts.
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                  LRQENGNVHAIA
                                                                             CGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVAVITVQLRRQYVRKYEGEABERKK
                                                                                                                                                                                           SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENT
                                                                                                                                                                                                               SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENT
                                                              CGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVAVITVQLRRQYVRKYEGEAEERKK
                                                                                                                            SDKPKRKKKGGKNGKNRRNRKKKNPCNAEFQNFCIHGBCKYIEHLEAVTCKCQQEYFGER
                                                                                                                                                                                                                                                            MRAPLLPPAPVVLSLLILGSGHYAAGLDLNDTYSGKREPFSGDHSADGFEVTSRSEMSSG
LRQENGNVHAIA
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Schilling
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Cherrington
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                                                                                                                                                                                                                                                                                                                                          Score 1308; DB 8; Pred. No. 2.2e-113;
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
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The invention relates to a combination comprising cDNAs that are differentially expressed in response to steroid treatment. Also included comprising cDNAs that are conference of the following: a high throughput method for using a cDNA to detect throughput method of screening molecules or compounds to identify a compound that specifically binds a cDNA. The sample; and a high compound that specifically binds a cDNA. The sample; are subject with conference of the combination with molecules or compounds to identify a disease and comparison of a standard defines a stage of that combination with molecules or compounds molecules or compounds specific binding; and detecting specific binding a cDNA comprises: combining compounds. The combination is useful for propounds under conditions to allow compounds. The combination is useful for propounds are regulatory correcting. The combination is useful for preparing a composition for compacting the compacting to a compound and at the compacting compounds are regulatory corrections. The present sequence represents a human protectin which is gequence data for this patent did not form part of the printed correction but was obtained in electronic format directly from Uspro
                                                                                                                                                                                                                                                                                                                                                                              Matches 252;
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 582; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Combination useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis, comprises cDNAs that are differentially expressed in response to steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-068610/07.
        241
                                     241
                                                                   181
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                                                                                                                 121 SDKPKRKKKGGKNGKNRKNRKKKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         steroid therapy; cirrhosis; hepatitis; human; C3A liver cell.
                                                                                                                                                                                          19
                                                                                                                                                                                                                                     LROENGNVHAIA
                  LRQENGNVHAIA
||||||||||
                                ČĠĖĸŚMŔTHŚMÍDŚŚLŚKĪĀLĀĀĪĀĀĒMŚĀVĪLTĀVĀVĪTVQLRRQYVRKYĒGĒĀĒĒRĶK 240
                                                      ŚDK PKRKKKK GGKNGKNRKNKKKKNPCNABPONPĆ I HGECKY I EHLEAVTCKĆOOBY PGER
                                                                                                                                                                         | SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIYDDSVRVEQVVKPPQNKTESENT 120
                                                                                                                                                     ŚĖIŚPVŚEMPSŚŚEPŚŚGADYDYŚEBYDNEPQIPGYIVDDŚVRVEQVVKPPQNKTEŚENT 120
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                                                                                                                                                                                                                  MRAPLLPPAPVVLSLLILGSGHYAAGLDLNDTYSGKREPPSGDHSADGFEVTSRSEMSSG
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ilarity 100.0%;
Conservative 0
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Pred. No. 2.2e-113;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                 252;
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RESULT

Query Match Best Local Similarity Matches 252; Conserv

100.0%; Score 1308; DB 8; Conservative 0; Mismatches 0;

Length

252; 0

Gaps

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The present invention describes a method of testing for bronchial asthma CC or chronic obstructive pulmonary disease. The method comprises from a subject, comparing the expression level of a marker gene in a biological sample compression level of the marker gene in a biological sample comparing the expression level determined with the compression level of the marker gene in a biological sample from a healthy obsert, and judging whether the subject has bronchial asthma or chronic cells are stimulated with interleukin-13, or (b) a group of cells are stimulated with interleukin-13, or (b) a group of cells are stimulated with interleukin-13, or (b) a group of the subject has bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent (I) for treat bronchial asthma or chronic obstructive pulmonary disease; (c) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (d) an inducer that induces bronchial asthma in a mouse; (5) a comethod for producing an animal model for bronchial asthma in a mouse; (5) a compound for a chronic obstructive pulmonary disease; (d) a therapeutic agent for obstructive pulmonary disease; (d) a the marker gene or an antisense nucleic acid corresponding to a portion of the gene through an RNAi effect or an antibody recognising compound asthma or a chronic obstructive pulmonary disease, compound, a protective pulmonary disease, a polynucleotide that suppresses the compound asthma or a chronic obstructive pulmonary disease, on which a protectival asthma or a chronic obstructive pulmonary disease, on which a for a cardial asthma or chronic obstructive pulmonary disease, on which a corresponding to a portion of corresponding to a portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Testing for bronchial asthma or chronic obstructive pulmonary disease becomparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-AUG-2002; 2002JP-00229312.
20-MAR-2003; 2003JP-00077212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENO-) GENOX RES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-AUG-2003; 2003EP-00254857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bronchial asthma; chronic obstructive pulmonary disease; respiratory epithelial cell; interleukin-13; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 819; 241pp; English.
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12-JUN-2002;
08-AUG-2002;
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13-AUG-2002;
22-AUG-2002;
04-OCT-2002;
                                                                                                                                                                                                                                                                                                     Rosen
Birse
    The invention preventing or
                                                                                                                                     New human secreted polypeptides and nucleic acid molecules for diagnosing, preventing or treating disorders associated with the secreted proteins, such as cancer, diabetes, obesity, cardiovascular disorders or
                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reproductive disorder; psoriasis; eczema; bronchitis; atherosclerosis; benign prostatic hyperplasia; asthma; Alzheimer'ë disease; Parkinson's disease; renal disord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; antidiabetic; anorectic; gynaecological; antipsoriatic; dermatological; antiarteriosclerotic; antiasthmatic; neuroprotective; nootropic; antipsrkinsonian; nephrotropic; human; secreted protein; diagnostic; pharmaceutical; cancer; lung; oesophageal; liver; diabete; obesity; metabolic disorder; cardiovascular disorder;
                                                                       Claim 1;
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DB; ADP07533.
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                                                                                                                                                                                                                                                                                                                             Ruben
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2002US-0388543P.
2002US-0401757P.
2002US-0402585P.
2002US-0402799P.
2002US-0404959P.
2002US-0415902P.
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GH, N
                                                                       English
  secreted polypeptide for diagnosing, associated with the secreted proteins.
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R, Shi Y;
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Best Local S
Matches 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polypeptides and nucleic acid molecules of the invention are useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating a medical condition. These may be used for diagnosing, preventing or treating disorders related to the human secreted proteins, such as cancer (e.g. lung, oesophageal or liver cancer), diabetes, obesity, metabolic disorders, cardiovascular disorders, reproductive disorders, psoriasis, eczema, bronchitis, cystic fibrosis, atherosclerosis, benign prostatic hyperplasia, asthma, Alzheimer's disease, Parkinson's disease or renal disorders. Sequences given in records for ADP07710-ADP07891 represent human secreted proteins of the
                                                                                                                       07-FEB-2003;
30-DEC-2003;
                                                                                                                                                           06-FEB-2004; 2004WO-US004176
                                                                                                                                                                                                           WO2004068931-A2
                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                       Antipsoriatic; cytostatic; gene therapy; amphiregulin; AR; heparin; PAR34; PAR80; HuPAR34; chimeric; humanised; antibody; cancer; psori
                                                                                                                                                                                                                                                                                                            Wild-type
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252; Conserv
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                                                                                                 PROTEIN DESIGN LABS INC.
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2003US-0533901P.
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Pred. No. 2.2
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2.2e-113;
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polypeptide, psoriasis.

New antibody that competitively inhibits binding of an amphiregulin polypeptide, useful for diagnosing or treating patients having cance

cancer

(AR)

WPI; 2004-653385/63.

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RESULT 9
ADDR67228
ADR6AXX
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                                                                                                                                             (HINZ/)
                                                                                                                                                                                                                26-FEB-2003; 2003DE-01009729
                                                                                                                                                                                                                                                        24-FEB-2004; 2004WO-DE000364.
                                                                                                                          (STAU/)
                                                                                                                                                                                                                                                                                                               10-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                   WO2004076613-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                    bladder cancer tissue; bladder cancer; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human bladder cancer associated amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADR67228 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an antibody that competitively inhibits binding of an amphiregulin (AR) polypeptide to an antibody. Ar is a heparining binding glycoprotein. The antibody comprises a heavy chain variable region having ammo acid sequence of at least 60% identity to a sequence selected from ADR73588, ADR73590 and ADR73598, and a light chain variable region having amino acid sequence of at least 60% identity to a sequence selected from ADR73589 and ADR73590. The antibody binds to the same AR epitope as that bound by an antibody selected from PAR34, and is chimeric or humanised. The antibodies are useful for diagnosing or treating patients having cancer and psoriasis. The current sequence represents the wild-type full-length human AR polypeptide.
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                                                       DAHL STAUB E.

PILARSKY C.

""RCHT T.
                                                                                                                HINZMANN B.
DAHL E.
STAUB E.
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                       Hinzmann B,
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                   Dah1
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                   'n
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              Staub
           'n
    Pilarsky C,
Specht
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AC CONTRACTOR ACCORDANCE OF AC
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AAG75109
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03-NOV-1999;
(HUMA-) HUMAN
                                                                                                         28-SEP-2000; 2000WO-US026524,
                                                                                                                                                                       05-APR-2001.
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Matches 252; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                     WO200122920-A2
                                                                                                                                                                                                                                                                                                      Human; colon cancer; colon cance: colorectal carcinoma; chromosome
                                                                                                                                                                                                                                                                                                                                                               Human colon cancer antigen protein SEQ ID NO:5873.
                                                                                                                                                                                                                                                                                                                                                                                                                                             03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG75109 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes nucleic acids (I) associated with bladder cancer tissue. Also described: (1) peptides and proteins (II) containing an amino acid sequence encoded by (I); (2) a method for diagnosing or agents (R); or monitoring its progression, that uses (I), (II) reporter; and (3) a method for treating BC that uses (I), (II) or (I) and (II) have cytostatic activity. (I) and (II) can be used to detect developing it; to screen for specific binding agents (Z), and to treat sequence represents a human amino acid sequence associated with bladder cancer, which is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                      Cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                   99US-0157137P.
99US-0163280P.
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100.0%; Pred. No. 2.2e-113;
tive 0; Mismatches 0;
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GENOME SCI INC

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coancer associated nucleic acid molecules (N) and proteins (P), where the CC proteins are collectively known as colon cancer antigens. The colon CC cancer antigens have cytostatic activity and can be used in gene therapy CC and treatment of diseases associated with inappropriate P expression. For CC example, N and P may be used in the prevention, diagnosis CC and treatment of diseases associated with inappropriate P expression. For CC example, N and P may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC supplement the activity of P by expressing inactive proteins or to CC supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids CC into a host cell and culturing the cell to express the proteins. N and P CC can be used in the prevention, diagnosis and treatment of colorectal CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent CC esquences used in the exemplification of the present invention. N.B.

CC Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027

CC time of publication, meaning no sequences are present for SEQ ID NO:1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
Human MCF 7 breast carcinoma cells
                                                                                                                                  27-AUG-2003
25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), wher
                              Amphiregulin; growth regulator; neoplastic immune response; arachidonic acid cascade.
                                                                                                                                                                                                                        AAP95447
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                                                                                Amphiregulin
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)B; AAH34514.
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ilarity 100.0%;
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(revised)
(first en
                                                                                precursor protein.
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Pred. No. 3.1e-113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colon cancer-associated polypeptides, and/or treating colorectal cancers.
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                                                disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326;
                                                resorption;
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RESULT 12 ADC71538 ID ADC71 XX ,

ADC71538

standard; protein;

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the precursor form of amphiregulin (ARPP). The corresp. DNA sequence is spliced to remove introns. The sequence is also processed to produce mature amphiregulin (AR). The mature protein is expressed using recombinant DNA methods and can be glycosylated or non-glycosylated. Abs can be produced which recognise an epitope of AR. AR is bifunctional growth regulator which inhibits growth of some cancers but stimulates growth of some normal cells. It is useful in the treatment diagnosis and monitoring of neoplastic diseases, for treating wounds etc. See also AAP90472, AAP90473, AAP90453, AAP90454, AAP90472, AAP90453, AAP90454, AAP90472, AAP90473, AAP90473, AAP90473, AAP90474, AAP90475, AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-1988;
15-APR-1988;
17-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New growth regulating proteins designated amphiregulin - inhibiting tumours but stimulating some normal cells, also new precursor prote encoding nucleic acid sequences and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1989-221730/31.
N-PSDB; AAN90373.
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                     241
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                                                                                                                                                                                                                                                                                                                                                                1 MRAPILPPAPVVLSILIIGSGHYAAGIDINDTYSGKREPFSGDHSADGFEVTSRSEMSSG
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BRISTOL-MYERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
LRQENGNVHAIA
                                                                                                                                                                                  SDKPKRKKKGGKNGKNRRNRKKKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGER
                                                                                                                                                                                                                                                                      SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKXPPQNKTESENT
                                                                                                    CGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVAVITVQLRRQYVRKYEGEABERKK
                                                                                                                                                                                                                                               SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPXNKTESENT
                                                                                                                                                                                                                                                                                                                                        MRAPLLPPAPVVLSLLILGSGHYAAGLDLNDTYSGKREPFSGDHSADGFEVTSRSEHSSG
                                                                                                                                                          SDKPKRKKKGGKNGKNRRNRKKKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mcdnald
                                                                                                                                                                                                                                                                                                                                                                                                                             99.0%;
ilarity 99.2%;
Conservative
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88US-00181884.
89US-00297816.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= amphiregulin
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                       252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  correct OS field.)
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Pred. No. 3.5e-112;
0; Mismatches 2;
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The present invention describes novel human proteins designated Novx, CC where X can be an integer of 1 to 7. The NovX protein and nucleotide CC where X can be an integer of 1 to 7. The NovX protein and nucleotide CC neuroprotective, nootropic, immunomodulator, antiparkinsonian, CC in gene therapy. The NovX proteins can be used in manufacturing a CC in gene therapy. The NovX proteins can be used in manufacturing a CC disease selected from a pathology associated with a human disease, the CC disease can be cancer. NovX proteins, nucleic acid molecules and CC disease can be cancer. NovX proteins, nucleic acid molecules and CC obseity, diabetes, metabolic disorders, nucleic acid molecules and CC diseases (e.g. Parkinson's disease or Alzheimer's disease). The CC diseases (e.g. Parkinson's disease or Alzheimer's disease), immune CC hyperkalaemia, hypoglycaemia, bone disorders and wasting disorders. The CC tissue typing, predictive medicine and pharmacogenomics. The present xx sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New NOVX polypeptides and nucleic acids for diagnosing, preventing treating NOVX-associated disorders, e.g. cancer, obesity, diabetes atherosclerosis, and for chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chant JS; Chapoval A, Chaudhuri A, Edinger SR, Eisen A, Gangolli EA; Gerlach VI, Guo X, Ji W, Khramtsov NV, Leite MW, Li L, Mezes PS; Millet I, Ooi CE, Ort T, Padigaru M, Patturajan M, Pena CEA; Rastelli L, Rieger DK, Quinn Senger KE, Smithson G, Spaderna SK; Spytek KA, Stone DJ, Twomlow N, Vernet CAM, Voss EZ, Zerhusen BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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07-AUG-2002;
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28-NOV-2001;
29-NOV-2001;
03-DEC-2001;
19-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; SEQ ID NO 166; 112pp; English.
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DB; ADC71537.
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1; 2001US-00996015
1; 2001US-0333912P
1; 2001US-0334300P
2; 2002US-0338196P
2; 2002US-0373806P
2; 2002US-0401593P
2; 2002US-0401593P
2; 2002US-00287190
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05-NOV-2001; 2001US-0338626P.
28-NOV-2001; 2001US-00996015.
28-NOV-2001; 2001US-033912P.
29-NOV-2001; 2001US-0334300P.
03-DEC-2001; 2001US-0338196P.
19-APR-2002; 2002US-0373806P.
16-MAY-2002; 2002US-0381043P.
07-AUG-2002; 2002US-0401593P.
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ADN33949
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                                             (ALSO/)
(ANDE/)
(BOLD/)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic disturbance; metabolic syndrome X; wasting disorder; antibacterial agent; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; NOVX; pancreatic polypeptide; angiopoietin; interleukin-1; endotepine; amphiregulin; metallocarboxypeptidase; metabolic disorder; diabetes; obesity; infectious disease; anorex; cancer; cancer-associated cachexia; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUN-2004
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) ALSOBROOK J I
) ANDERSON D W.
) BOLDOG F L.
) BURGESS C E.
) CHANT J S.
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polymorphism"
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Pred. No. 8.8e-106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleotide
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CHAPOVAL A.

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The invention relates to 87 isolated NOVX polypeptides (NOV1-NOV5), their CC mature forms and their encoding polynucleotides having sequence CC similarity to pancreatic polypeptide (NOV1), angiopoletin (NOV2), CC interleukin-1 (NOV2), endothelin-2 (NOV4), endozepine (NOV5), and metallocarboxypeptidase (NOV7). Also included the use of NOVX in the manufacture of a medicament for treating a human CC disease associated with NOVX, detecting NOVX in a sample via an CC immunoassay, identifying an agent that binds to the NOVX polypeptide, CC modulating the activity of NOVX, a vector comprising NOVX polypeptide, CC a cell comprising the vector, an antibody that immunospecifically binds to NOVX, detecting the polypeptide or emprising the cell under CC conditions that lead to expression of the polypeptide. NOVX and its CC conditions that lead to expression of the polypeptide. NOVX and its polypeptides e.g. metabolic disorders, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX CC polypeptides e.g. metabolic disorders, diabetes, obesity, infectious CC disease, anatexia, cancer-associated cachexia, neurodegenerative CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders, hadeiners and the various dyslipidaemias, metabolic condition of antigen in the production of antibodies and various cancers. They may also be used as antibacterial agents. NOVX may also be used as CC an antigen in the production of antibodies and in assays to identify of NOVX. The present sequence represents a NOVX protein.
XCCCCCCCCCCCCCCCCCCCCCCCCCXPXTTXRRXIIIIIIIIIIIIIIIIIIIIIIIIIIIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chant JS; Chapoval A, Chaudhuri A, Edinger SR, Bisen A, Gangolli EA; Gerlach V, Guo XS, Ji W, Khramtsov NV, Leite MW, Li L, Mezei Millet I, Ooi CE, Ort T, Padigaru M, Patturajan M, Pena CEA; Rastelli L, Rieger DK, Senger KEQ, Smithson G, Spaderna SK; Spytek KA, Stone DJ, Twomlow N, Vernet CAM, Voss EZ, Zerhusei
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing
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(VOSS/)
(ZERH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SPAD/)
(SPYT/)
(STON/)
(TWOM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RAST/)
(RIEG/)
(SENG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL/)
(OOIC/)
(ORTT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's diseas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PADI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (JIWW/)
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(CHAU/)
(EDIN/)
(EISE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2004-213932/20.
DB; ADN33948.
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PATTURAJAN M.
PENA C E A.
RASTELLI L.
RIÈGER D K.
SENGER K E Q.
SMITHSON S K.
SPADERNA S K.
SPYTEK K A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDINGER S R.
EISEN A.
GANGOTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MILLET I.
OOI C E.
ORT T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STONE D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZERHUSEN B D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEZES P S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GANGOLLI E A. GERLACH V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZHONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KHRAMTSOV N
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                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 166; 129pp; English
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27 LDLNDTYSGKREPFSGDHSADGFEVTSRSEMSSGSEISPVSEMPSSSEPSSGADYDYSEE

Matches

Conservative

0

Mismatches

Indels

0; . Gaps

86

Query Match Best Local Similarity

90.0%;

Score 1177; DB 2; Pred. No. 3.1e-101;

Length

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RESULT 14
ANAT73157
ID ANAT73
XX ANAT73
XX 20-JP
XX Amphi
PR 15-JP
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                                                                 This sequence represents the human amphiregulin (AR) transmembrane glycoprotein of the invention. The invention also relates to rat, and bovine AR proteins. The AR proteins can be used to stimulate epithelial cell growth. They may be of therapeutic use in controll tumour cell growth and in disorders such as psoriasis, and can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
  Sequence
                                                   a tumour
                                                                                                                                                                                                            Claim 11;
                                                                                                                                                                                                                                                                                Amphiregulin proteins -
                                                                                                                                                                                                                                                                                                                                 WPI; 1998-609313/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-1988;
17-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5830995-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human amphiregulin transmembrane glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW73157 standard;
                                                                                                                                                                                                                                                                                                                                                                               Plowman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amphiregulin; AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW73157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLILGSGHYAAGLDLNDTYSGKREPFSGDHSADGFEVTSRSEMSSGSEISPVSEMPSSSE
                                                marker tor
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    226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSSGADYDYSEEYDNEPQI PGYI VDDSVRVEQVVKP PQNKTESENTSDKPKRKKKGGKNG
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                                                                                                                                                                                                            Col 71-72;
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    A,
                                                                                                                                                                                                                                                                                                                                                                             Bradley
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88US-00181884.
89US-00297816.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                              cancer diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry
                                                                                                                                                                                                            76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.7%;
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                                                                                                                                                                                                                                                                                   useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epithelial cell growth; tumour cell growth; cancer diagnosis; therapy; human.
                                                                                                                                                                                                                                                                                                                                                                             Shoyab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226
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Pred. No. 8.8e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                             8
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                                                                                                                                                                                                                                                                                stimulating e.g. epithelial
                                                                                                                                                                                                                                                                                                                                                                               Mcdonald
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                                                                                              controlling
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                                                                                                                                             mouse
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RESULT 15
AAW73160
ID AAW73
XX AAW73:
XX AAW73:
XX AAW73:
XX AAW73:
XX AAW74:
XX AAWphi
AX AAWph
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                                                                                                                                                                                          Query Match
76.8%; Score 1004.5; DB 2; Length
Best Local Similarity 77.5%; Pred. No. 4.3e-85;
Matches 196; Conservative 19; Mismatches 31; Indels
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                                                                                                                                                                                                                                                                                                                         This sequence represents the bovine amphiregulin (AR) of the invention. The invention also relates to rat, mouse and human AR proteins. The AR proteins can be used to stimulate epithelial cell growth. They may be of the therapeutic use in controlling tumour cell growth and in disorders such as psoriasis, and can be used as a tumour marker for cancer diagnosis
                                                                                                                                                                                                                                                                                                            Sequence 247 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-1988;
15-APR-1988;
17-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig la; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amphiregulih proteins - useful for stimulating e.g. epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-609313/51.
N-PSDB; AAV59098.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAY-1992;
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                            61 SBISPVSEMPS88EPS8GADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENT 120
                                                                                      ŚETPĖGGĖL-----ŚSVIDYDYAŁEYDNEPQISGYIVDDŚVRVEQVVKPKKKKTĖSEKT
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88US-00181884.
89US-00297816.
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DЪ	Ş	뮍	γQ	DЬ	δ
235	240	175	181	115	121
KLRQENGNAHAVA 247	240 KLRQENGNVHAIA 252	175 CGEKSMKTQSMVDSDLSKIALAAIAAFVSAMWETATAVETTIII :	181 CGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVAV-TTVOI BEOVETESIEGEK 174	SDKPKRKKKGGKNGKNRRNRKKKNICOTEPONFCIHGKCTFLFOIETVSCOCYPTYSTER	SDKPKRKKKGGKNGKNRRNRKKKNPC

Search completed: February 26, 2005, 16:41:14 Job time : 167 secs

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Minimum DB
Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
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                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0 seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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                     US-09-919-039-228
US-10-1177-293-13
US-10-301-822-8
US-10-440-464-51
US-10-106-698-5883
US-10-287-190-166
US-10-022-609-15
US-10-022-609-16
US-10-021-609-16
US-10-021-609-16
US-10-009-370-114
US-10-096-241-18
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              Sequence 2, Appli
Sequence 28, App
Sequence 13, Appl
Sequence 8, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 166, Appl
Sequence 166, Appl
Sequence 16, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 16, Appl
Sequence 11, Appl
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145	145	145	145	145	145	145	145	145	145	145	145	145	145	163	166	166	184.5	197	211.5	211.5	211.5	211.5	211.5	211.5	211.5	211.5	211.5	231	263	263	263
11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.1	12.5	12.7	12.7	14.1	15.1	16.2	9	16.2	9	9	•	•	16.2	16.2	17.7	$\dot{\mathbf{a}}$	20.1	20.1
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US-10-144-678A-590	US-10-012-896-590	US-09-895-814-590	บร-09-895-793-590	US-09-822-827-590	US-09-780-669-590	US-09-759-143-590	US-10-294-025-940	US-10-144-678A-940	US-10-012-896-940	US-09-895-814-940	US-09-895-793-940	US-09-822-827-940	US-09-780-669-940	US-10-022-609-17	US-10-106-698-5940	US-10-189-360-6	US-10-189-360-8	US-08-736-019-153	US-10-868-577A-51	US-10-868-577A-46	US-10-868-577A-22	10-428	US-10-395-540-2	ب	H	US-10-138-158-18	10-096-327-	μ.	US-10-215-862-10	-10-136-573	US-09-877-665-10
590,	e 590,	590,	590,	590,	590,	Sequence 590, App	Sequence 940, App	Sequence 940, App	m				Sequence 940, App	Sequence 17, Appl	Sequence 5940, Ap		e 8,	153,	ហ	46,	22,	38,	'n	7,	ហ	18,	,	13	e 10	e 10	Sequence 10, Appl

ALIGNMENTS

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NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL PROGRAM
SEQ ID NO 2
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020156263A1 3478236CD1
US-09-974-298-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-974-298-2
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Fatent No. US20020156263A1
GENERAL INFORMATION:
APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT APPLICATION NUMBER: 001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR PILING DATE: 2000-05-10
                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                     Local Similarity
nes 252; Conserv
121 SDKPKRKKKGGKNGKNRRNRKKKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGER 180
                                            61 SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENT
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                                                                       SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENT
                                                                                                                                          MRAPLIPPAPVVLSLLILGSGHYAAGLDLNDTYSGKREPFSGDHSADGFEVTSRSEMSSG
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                                                                                                                                                                                                                                                                                 DB 9; Length 252;
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Sequence 13, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gannawarpu, Manjula
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
                                                                                                                                                                                                                                                                RESULT 3
US-10-177-293-13
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FEATURE:
NAME/KEY: misc feature
OTHER INFORMATTON: Incyte ID No. US20030108871A1 3478236CD1
US-09-919-039-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 252; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SÓKÞKRKKKGGKNGKNRKNRKKKKNÞCNABFONÞCÍHGECKYÍBHLEAVTCKCOOEVFGER 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENT 120
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ilarity 100.0%;
Conservative 0
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5. US20030108871A1
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Sequence 8, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, In
APPLICANT: Millennium Pharmaceuticals, In
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
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SEQ ID NO 13

LENGTH: 252

TYPE: PRT

CRGANISM: Homo sapiens

US-10-177-293-13
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APPLICANT: MILLS, GOTGON B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND
FILE REFERENCE: MAI-038
CURRENT APPLICATION UNMBER: US/10/177, 293
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR PILLING DATE: 2001-06-21
PRIOR PILLING DATE: 2001-06-27
PRIOR PILLING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR APPLICATION NUMBER: US 60/362,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 252;
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Best Local
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Meyers, Rachel E.
Bast Jr., Robert C.
Hortobagyi, Gabriel N
Pusztai, Lajos
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APPLICANT: CHERRINGTON, JULIE
APPLICANT: SCHILLING, JIM
ITTLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
ITTLE OF INVENTION: AND ACTIVITY IN MAMMALS
ITTLE OF INVENTION: AND ACTIVITY IN MAMMALS
CURRENT APPLICATION NUMBER: US/10/440,464
CURRENT APPLICATION NUMBER: 60/380,872
PRIOR APPLICATION NUMBER: 60/48,972
PRIOR APPLICATION NUMBER: 60/448,922
PRIOR APPLICATION NUMBER: 60/448,922
PRIOR APPLICATION NUMBER: 60/448,922
PRIOR APPLICATION NUMBER: 60/448,874
PRIOR FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 185
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 5: 185
SEQ ID NO 5: 185
SEQ ID NO 5: 252
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US-10-440-464-51
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CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
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Best Local Similarity 100.0%;
Matches 252; Conservative 0
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SEQ ID NO 8
LENGTH: 252
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APPLICANT: O'FARRELL, ANNE-MARIE
APPLICANT: MORIMOTO, ALYSSA
APPLICANT: MOLICH, BEVERLY
APPLICANT: MANNING, WILLIAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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Pred. No. 2.9e-110;
D; Mismatches 0;
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; ORGANISM: Homo sapiens US-10-106-698-5883
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US-10-106-698-5883
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; ORGANISM: Homo
US-10-440-464-51
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Matches
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SOPTWARE: PatentIn Ver. 3.0
SEQ ID NO 5883
LENGTH: 326
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                          Query Match
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TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1909-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR PRILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
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Best Local
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CGEKSMKTHSMIDSSLSKIALAAIAAAFMSAVILTAVAVITVQLRRQYVRKYEGEAEERKK
                                                                                   SDKPKRKKKGGKNGKNRKKKKNPCNASFQNFCIHGECKYIEHLEAVTCKCQQEYFGER
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100.0%; Pred. No. 2.9e-110;
tive 0; Mismatches 0;
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RESULT 8
US-10-022-609-15
VS-10-022-609-15
Sequence 15, Application US/10022609
Publication No. US20030023035A1
GENERAL INFORMATION:
GENERAL INFORMATION:
Candlen Richard L
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PRIOR FILING DATE: 2002-08-07
PRIOR PRIOR PAPLICATION UNMBER: 60/334300
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEG ID NOS: 194
SEOTMARE: CuraSeqList version 0.1
SEO ID NO 166
LENGTH: 235
TYPE: PRT
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CURRENT FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: 09/996,015
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/338626
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/338196
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/338196
PRIOR APPLICATION NUMBER: 60/338196
PRIOR APPLICATION NUMBER: 60/338196
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/333912
PRIOR FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alsobrook II, John P. et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD PROPERTIONS OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENERAL INFORMATION:
                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
                                                                                                                                                             TITLE OF INVENTION: Structure, F
                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity es 235; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/381043
FILING DATE: 2002-05-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SĹSKÍAĹĀĀĪĀĀĒWSĀVĪĹTĀVĀVĪTVOLKĶOŢVĶĶŢĒĢĒĀĒĒĶĶĶĻĶĢĒNGNVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SISKIALAAIAAFMSAVILTAVAVITVOLRRQYVRKYEGEAEERKKLRQENGNVH 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNRKNRKKKNPCNABPONPCIHGECKYIBHLEAVTCKCQQBYFGERCGEKSNKTHSNIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PŚŚĆADYDYŚEBYDNEPOTPGYTVDDŚVRVEOVVKPPONKTBŚENTSDKPKKKKKGKNG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 LRQENGNVHAIA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSŚGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENTSDKPKRKKKGGKNG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĹĹĬĹĠŚĠĦŸĀĠĠĹĎĹŃĎŤŸŚĠĸĸĔPŦŚĠĎĦŚĀĎĠŦĖVŤŚŔŚĒMSŚĠŚĒĬŚPVŚĔMPŚŚŚĒ
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.__US20040038230A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.7%; Score 1226; DB 15;
100.0%; Pred. No. 7.3e-103;
tive 0; Mismatches 0;
                                                                                                                                                                               Production and Use of
                                                                                                                                                                Ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 235;
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US-10-022-609-16
; Sequence 16, Application US/10022609
; Publication No. US20030023035A1
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb :
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 712C:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATE: US/08/440,401
APPLICATION NUMBER: US/08/440,401
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: 08/330161
FILING DATE: 25-OCT-1994
APPLICATION NUMBER: 08/035430
FILING DATE: 22-MAX-1993
APPLICATION NUMBER: 07/705256
APPLICATION NUMBER: 07/705256
FILING DATE: 24-MAY-1991
                                                                                                                                                                                                                                                                                                                                            HOIMES, ....- FITTLE OF INVENTION: Structure, F
                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Vandlen, Richard L.
Holmes, William E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 LAAIAAFMSAVILTAVAVITVQLRRQY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 KKKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGERCGEKSMKTHSMIDSSLSKIA 200
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 100.0%;
87; Conservative

    KKŃPCNASPONFCIHGECKYIEHLEAVTCKĆOÓEYFGERCGEKSNKTHSMIDSSLSKIA

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FILING DATE: 17-Dec-2001
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>,</u>
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; Pred. No. 1.9e-33;
                                                                       360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                              Production and Use
                                                                                                                                                                                                                                                                                                                                            Ligands
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Gaps

CURRENT APPLICATION DATA:

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US-10-201-945-11
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Publication Nd. US20020188110A1
GENERAL INFORMATION:
APPLICANT: Meissner, Paul S.
Fildner, Rebecca A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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THLEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 71:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
           APPLICATION NUMBER: US/10/201,945
FILING DATE: 25-Jul-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/471,377
FILING DATE: 23-Dec-1999
APPLICATION NUMBER: 08/915,096
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams, Mark D.
TITLE OF INVENTION: Transforming Growth Factor Alpha NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 KKKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGERCGEKSMKTHSMIDSSLSKIA 200
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FILING DATE: 12-MAY-1995
APPLICATION NUMBER: 08/330161
FILING DATE: 25-OCT-1994
APPLICATION NUMBER: 08/035430
FILING DATE: 22-MAR-1993
APPLICATION NUMBER: 07/705256
FILING DATE: 24-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAAIIVEVSAVSVAAIGIITAVLLRK 86
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                                                                                                                                                                                                                                                                                                                                              STATE: MD
                                                                                                                                                                                                                                                                                                                                                                  CITY: Rockville
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                                                                                                                                                                                                                                                                                                    ZIP: 20850
                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 87 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.5%;
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; Pred. No. 2.7e-21;
10; Mismatches 17;
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APPLICANT: Young et al.
TITLE OF INVENTION: Heregulin-Like Factor
FILE REFERENCE: PF383D1
CURRENT APPLICATION NUMBER: US/10/609,370
CURRENT FILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: 09/097,681
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/049,942
PRIOR APPLICATION NUMBER: 50/049,942
PRIOR FILING DATE: 1997-06-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
                                                                                                                                                                                                                                       RESULT 12
US-10-096-241-18
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US-10-609-370-14
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US-10-609-370-14
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                                                                                                                                                                      Sequence 18, Applicati
Publication No. US2002
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.6%; Score 283; DB 15; Best Local Similarity 100.0%; Pred. No. 2.9e-18; Matches 49; Conservative 0; Mismatches. 0;
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             NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
                                                                                 Busfield, Samantha J.
TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
AND USES THEREFOR
                                                                                                                          APPLICANT: Gearing, David P.
Busfield, Samanth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF110D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             140 RKKKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGERCGEKSMKT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 KWRRNRKKKWPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGERCGEKSM 186
                                                                                                                                                                                                                                                                                                                                 1 RKKKNPCNAEFONFCIHGECKYIEHLEAVTCKCQQEYFGERCGEKSMKT 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 52 amino acids
TYPE: amino acid
STRANDEDENESS: single
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 301-309-8504
TELEX: 301-309-8439
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                                                                                                                                                                                                                  Application US/10096241
                                                                                                                                                                                             US20020127594A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.9%; Suc. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Part. Eav
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; Pred. No. 9.1e-20;
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Length 45; Indels

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RESULT 13
US-09-817-647-10
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SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-096-241-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09817647
Patent No. US20020082229A1
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.5%; Sc Best Local Similarity 100.0%; I Matches 46; Conservative 0;
                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

APPLICATION INDER: US/09/817,647

PILING DATE: 26-Mar-2001

CLASSIFICATION - Unknown>

PRIOR APPLICATION DATA:

CLASSIFICATION - Unknown>

PRIOR APPLICATION OATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                        ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/096,241
FILING DATE: 12-Mar-2002
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related
Ligands and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 KKKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGERCGEKSM 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: FASSE, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07334/022001
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/699,591

FILING DATE: 19-AUG-1996

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KKKNPCNÁBPÓNPCTHGECKYTEHLBÁVTCKCÓÓBÝPGERCGEKSM 46
                                                                      APPLICATION NUMBER: 09/107,979 FILING DATE: <Unknown>
                  NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
                                                                                                                                                                                                                                                                                                                                   STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
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COUNTRY: US
ZIP: 02110-2804
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; Pred. No. 6.2e-17;
0; Mismatches 0;
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US-09-877-665-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09877665
Patent No. US20020164680A1
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-817-647-10
                                                                                                                             INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 45 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
APPLICATION LOTA:
APPLICATION NUMBER: US/09/877,665
FILLING DATE: 08-Jun-2001
PRIOR APPLICATION ON : (Unknown)
PRIOR APPLICATION NUMBER: US/09/109,206
FILLING DATE: 30-Jun-1998
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1-1
TELEPHONE: 650/225-2066
TRI.REAY. KEN/ASZ-0201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                        FEATURE:
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CORRESPONDENCE ADDRESS:
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TELEPHONE: 650/225-2066
                    LOCATION: 1-45
IDENTIFICATION METHOD:
OTHER INFORMATION:
                                                          NAME/KEY: har.egf
LOCATION: 1-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KKNPCNÁEFONFCÍHGECKYÍEHLEAVTCKCÓÓEYFGERCGEKSM 45
                                                                                                                   TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
45; Conserv
                                                                                                                                                                                                       TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: South San FI
STATE: California
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OTHER INFORMATION:
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LOCATION:
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LENGTH: 45 amino acids
TOPE: Amino Acid
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: 1 San Francisco
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100.0%; Pred. No. 1.7e-16;
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APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Zhang, Dong Xiao
ITITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and
ITITLE OF INVENTION: Uses Therefor
FILE REFERENCE: P1084R1C2
CURRENT APPLICATION NUMBER: US/10/136,573A
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 09/480,977
PRIOR PILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: US 08/899,437
PRIOR APPLICATION NUMBER: US 08/899,437
PRIOR FILING DATE: 1997-07-24
PRIOR FILING DATE: 1997-07-24
PRIOR FILING DATE: 1997-07-09
INUMBER OF SEQ ID NOS: 23
SEQ ID NO 10
LENGTH: 45
TYPE: PAT
ORGANISM: Homo sapiens
US-10-136-573A-10
Search completed: February 26, 2005, 16:56:18 Job time : 136 secs
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US-10-136-573A-10
                                                                                                                                                                                                          Query Match 20.1%; Score 263; DB 13; Length 45; Best Local Similarity 100.0%; Pred. No. 1.7e-16; Matches 45; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/10136573A Publication No. US20020161200A1 GENERAL INFORMATION:
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                                                                                                                                       142 KKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGERCGEKSM 186
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                                                                                                     1 KKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGERCGEKSM 45
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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182.5
142.5
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137
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seq length: 2000000000
      14.12
112.4.1
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1308
1 MRAPLLPPAPVVLS
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1: pir1:*
2: pir2:*
3: pir3:*
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Match
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Gapop 10.0 ,
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heparin-binding EG
heparin-binding EG
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epidermal growth f	neu differentiation	growth factor - va	heregulin, splice	F14L17.4 protein	hypothetical prote	neu differentiation	sensory/motor neur	neu differentiatio	hypothetical proto	CDEI-box DNA-bind:	epidermal growth	neu differentiat	DNA-directed RNA	heregulin precurso	

ALIGNMENTS

C;Genetics: A;Gene: GDB;AREG A;Cross-references: GDB;119697; OMIM:104640 A;Cross-references: GDB;119697; OMIM:104640 A;Map position: 4q13-4q21 A;Introns: 21/1; 104(1; 171/1; 222/2 C;Superfamily: amphiregulin; EGF homology C;Keywords: extracellular procein; glycoprotein; growth factor; transmembra: F;1-19/Domain: signal sequence #status predicted <sig> F;1-19/Domain: propeptide #status predicted <pro> F;101-184/Product: amphiregulin long form #status experimental <mal> F;107-184/Product: amphiregulin short form #status experimental <mas> F;116-181/Domain: EGF homology <egf></egf></mas></mal></pro></sig>	A;Cross-references: GB:M30704; NID:g179039; PIDN:AAA51781.1; PID:g179040 R;Shoyab, M.; Plowman, G.D.; McDonald, V.L.; Bradley, J.G.; Todaro, G.J. Science 243, 1074-1076, 1989 A;Title: Structure and function of human amphiregulin: a member of the epidermal A;Reference number: A30057; MUID:89162036; PMID:2466334 A;Recession: A30057 A;Molecule type: protein A;Residues: 101-112,'D',114-184 <sh1> R;Shoyab, M.; McDonald, V.L.; Bradley, J.G.; Todaro, G.J. Proc. Natl. Acad. Sci. U.S.A. 85, 6528-6532, 1988 A;Title: Amphiregulin: abjuictional growth-modulating glycoprotein produced A;Reference number: A94205; MUID:88320474; PMID:3413110 A;Accession: A31230</sh1>	amphiregulin precursor [validated] - human C;Species: Homo sagiens (man) C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004 C;Accession: A34702; B34702; A30057; A31230; A39788; A30056 C;Accession: A34702; B34702; A30057; A31230; A39788; A30056 R;Plowman, G.D.; Green, J.M.; McDonald, V.L.; Neubauer, M.G.; Disteche, C.M., Tox Mol. Cell. Biol. 10, 1969-1981, 1990 A;Title: The amphiregulin gene encodes a novel epidermal growth factor-related p. A;Reference number: A34702; MUID:90220581; PMID:2325643 A;Accession: A34702 A;Molecule type: DNA A;Residues: 1-252 <pli> A;Cross-references: UNIPROT:P15514; GB:M30698 A;Accession: B34702 A;Molecule type: mRNA A;Residues: 1-252 <pli> A;Accession: B34702 A;Molecule type: mRNA A;Residues: 1-252 <pli> A;Accession: B34702</pli></pli></pli>

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A;Residues: 1-248 < DAS.

A;Cross references: GB:141352; NID:9845598; PIDN:AAB00472.1; PID:9845599

A;Cross references: GB:141352; NID:9845598; PIDN:AAB00472.1; PID:9845599

C;Comment: Amphiregulin is a secreted protein that is released from the transmembrane process; Superfamily: amphiregulin; EGF homology

F;10-93/Domain: signal sequence #status predicted < SIG.

F;10-17/Product: amphiregulin long form #status predicted < MAL.

F;192-17/Domain: EGF homology < SGP.

F;192-217/Domain: transmembrane #status predicted < MAL.

F;192-248/Domain: intracelluare #status predicted < MAS.

F,106/Binding site: carbohydrate #status predicted < MAS.

F,107-163,165-174/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Molecule type; mRNA; Residues; 1-248 <SONs; Residues; NID: Residues; Resi
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// Alternate names: Schwannoma-derived growth factor precursor
// Species: Mus musculus (house mouse)
// Alternate names: Schwannoma-derived growth factor precursor
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1 MRAPLLPPAPVVLSLLILGSGHYAAGLDLNDTYSGKREPFSGDHSADGFEVTSRSEMSSG 60
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heparin-binding EGF-like growth factor precursor - human C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change R;Higashiyama, S.; Abraham, J.A.; Miller, J.; Fiddes, J.C.; Klag Science 251, 936-939, 1991
A;Title: A heparin-binding growth factor secreted by macrophage-
                                                                                                                                                                                                                               RESULT 4
A38432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-243 < KIM>
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Best Local (
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;Superfamily: amphiregulin; EGF homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŚĖVŚTIŚEMPŚGŚĖLŚTG-DYDYSEEYDNĖPOISOYIVDDŚVRVĖOVIKPKENKTĖGĖKS
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                          Abraham, J.A.; Miller, J.; Fiddes, J.C.; Klagsbrun, M.
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69.7%; Pred. No. 5.1
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pinding growth factor secreted by macrophage-like cells that is

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A;ACCCCOPATHORMA
A;Molecule type: mRNA
A;Residues: 1-208 <HOO>
C;Comment: This precursor is a transmembrane glycoprotein which is c
C;Comment: This precursor is a transmembrane growth factor; EGF homology
C;Keywords: receptor; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;63-150/Product: diptheria toxin receptor precursor #status predicted:
F:108-143/Domain: EGF homology <EGF>
F:108-143/Domain: Heattus predicted <TRN>
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A41914
A41914
diptheria toxin receptor precursor - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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R;Hooper, K.P.; Eidels, L.
Biochem. Biophys. Res. Commun. 220, 675-680, 1996
A;Title: Glutemic acid 141 of the diptheria toxin receptor (HB-EGF A;Reference number: JC4687; MUID:96183008; PMID:8607824
A;Accession: JC4687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell 169, 1051-1061, 1992
A;Title: Expression cloning
A;Reference number: A41914;
A;Accession: A41914
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C; Superfamily: h
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A; Residues: 63-74,'X',76-84,'X',86-148 <HI2>
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Best Local
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;Residues: 1-208 <HIG>
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                                                                                                                                                                                 Similarity 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 16.2%;
Similarity 36.7%;
                                                                                                  DSVRVEQVVKPPQNKTESENTSDKPKRKKKGGKNGKNRRNRKKKNPCNAEFQNFCIHGEC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGLLMFRYHRRGGYDVENEEKVKLGMTNSH 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVQLRRQYVRK--YEGEAEERKKLRQENGN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYIEHLEAVTCKCQQEYFGERCGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVAVI 219
                               DLLRVTLSSKPQALATPSK--EEHGKRKKKGKGLG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KYVKELRAPSCICHPGYHGERCHGLSLPVENRLYTYDHTTILAVVAVVLSSVCL----LVI
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                                                                                                                                                                             16.2%; Score 211.5; DB 1; 36.7%; Pred. No. 2.3e-09; tive 24; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of a diphtheria toxin receptor: identity with a MUID:92298386; PMID:1606612
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Pred. No. 2.3e-09;
3; Mismatches 59;
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A;Residues: 1-208 <ABR>
A;Cross-references: UNIPROT:Q06175; GB:L05489; NID:g204289; PIDN:AAA81780.1;
A;Cross-references: UNIPROT:Q06175; GB:L05489; NID:g204289; PIDN:AAA81780.1;
C;Superfamily: heparin-binding EGF-like growth factor; EGF homology
C;Keywords: growth factor; heparin binding; transmembrane protein
C;Keywords: growth factor; heparin binding; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
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RESULT 7
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Gene 16, 291-292, 1996
A;Title: Characterization of the gene encoding murine heparin-binding epiderm A;Reference number: JC4659; MUID:96194822; PMID:8647467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Abraham, J.A.; Damm, D.; Bajardi, A.; Miller, J.; Kla. Biochem. Biophys. Res. Commun. 190, 125-133, 1993 A;Title: Heparin-binding EGF-like growth factor: Charac A;Reference number: JC1409; MUID:93135756; PMID:7678488 A;Accession: JC1410
                                                                                                                                         heparin-binding EGF-like growth factor precursor - C;Species: Rattus norvegicus (Norway rat) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 16/1; 74/1; 133/2; 185/2
C;Superfamily: heparin-binding EGF-like growth factor; EGF homolog C;Keywords: growth factor; heparin-binding; transmembrane protein F;1-23/Domain: signal sequence #status predicted <SIG>F;24-208/Product: heparin-binding EGF-like growth factor #status F;108-143/Domain: EGF homology <EGF>
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A;Title: Heparin-binding EGR
A;Reference number: JC1409;
A;Accession: JC1409
                                                                        Biochem. Biophys.
                                                                                                  R;Abraham,
                                                                                                                         C; Accession: JC1409
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A;Residues: 1-208 <HAR>
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Best Local
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                       J.A.; Damm, D.; Bajardi, A.; Miller, J.; Klagsbrun, M.; Slophys. Res. Commun. 190, 125-133, 1993 leparin-binding EGF-like growth factor: Characterization to number: JC1409; MUID:93135756; PMID:7678488
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                                                                                                                                                                                                                                                                                                                                                                             184 KSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVAVITVQLRRQYVRK--YEGEAEBRKKL
                                                                                                                                                                                                                                                                                                                                                                                                                              86
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                                                                                                                                                                                                                                                                                                                            LTLPVENPLYTYDHTTVLAVVAVVLSSVCL---LVIVGLLMFRYHRRGGYDLESEEKVKL
                                                                                                                                                                                                                                                                                                                                                                                                                            PSKERNGKKKKKGKGLGKKRDPCLRKYKDYCIHGECRYLQEFRTPSCKCLPGYHGHRCHG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKRKKKGGKNGKNRRNRKKKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGERCGE 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 185.5; DB 1;
Pred. No. 2.5e-07;
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                                                                                                                                                 #text_change 09-Jul-2004
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G01639
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C;Keywords: growth factor; he
F;10-45/Domain: EGF homology
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S27162; S25158
R;Vaughan, T.J.; Pascall, J.C.; Brown, K.D.
Biochem. J. 287, 681-684, 1992
A;Title: Tissue distribution of mRNA for heparin-binding epidermal growth f; A;Reference number: S27162; MUID:93075016; PMID:1445231
A;Paccession: S27162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q01580; EMBL:X67295; NID:g1969; PIDN:CAA47709.1; C;Superfamily: heparin-binding EGF-like growth factor; EGF homology C;Keywords: growth factor; heparin binding F;10-45/Domain: EGF homology <EGF>
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A; Residues: 1-84 < VAU>
                                                                                                                                                                                                                                                                                                                                                  ransmembrane protein - human ;Species: Homo sapiens (man) ;Date: 21-Dec-1996 #sequence_revision
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Best Local
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                                                                                                                                                                                   Cross-references: UNIPROT:Q13086; EMBL:U19878; NID:g755465; PIDN:AAA64622.1; PID:g7554
                                                                                                                                                                                                                     ;Molecule type: mRNA
;Residues: 1-380 <EI
                                                                                                                                                                                                                                                                                                                            ;Accession: G01639
;Eib, D.W.
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Best Local S
Matches 29
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F;108-143/Domain:
F;161-184/Domain:
                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 KSMKTHSMIDSSLSKIALAAIAAFWSAVILTAVAVITVQLRRQYVRK--YEGEAEERKKL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 PKRKKKGGKNGKNRRNRKKKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGERCGE 183
                                                                                                                                                                                                                  1-380 <EIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ຫ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 PGKEKNGKKKRKGKGLGKKRDPCLKKYKDYCIHGECRYLKELRIPSCHCLPGYHGQRCHG 145
                                                                                                                                 Similarity
   GSEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDS-VRVEQV-VKPPQNKTES 117
                                   ARGPCYSDNGSGSGE----GEEEGSGAEVHRKHSKCGPCKYKAECDEDAENVGCVCNIDCS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                           AAGLDLNDTYSGKREPFSGDHSADGFEVTSRSEM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAVVAVVLSSVCLLVI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLPVENPLYTYDHTTVLAVVAVVLSSVCL---LVIVGLLMFRYHRRGGYDLESEEKVKL
                                                                                                                 Conservative
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                                                                                                                             11.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.4%;
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                                                                                                                          Score 144.5; DB 2
Pred. No. 0.00076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 162; DB 2;
Pred. No. 6.1e-06;
7; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 184.5;
Pred. No. 2.9
                                                                                                                                                                                                                                                                                                   January
                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .9e-07;
                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 84;
                                                                                                        Indels
                                                                                                                                        Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                          55;
                                                                       -----SS 59
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                                                                                                    Gaps
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Query Match
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A;Molecule type: DNA
A;Residues: 1-141 <LOU>
A;Residues: 1-141 <LOU>
A;Cross-references: UNIPROT:Q28218; EMBL:X89728; NID:g1052560; PIDN:CAA61880.1;
C;Superfamily: heparin-binding EGF-like growth factor; EGF homology
                                                                                                                                                             EGF-like growth factor, precursor - green monkey Grivet) (Species: Cercopithecus aethiops (green monkey, grivet) C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change C;Accession: S58117 R;Loukianov, E.V.; Loukianov, T.I.; Wiedlocha, A.; Olsnes, S. submitted to the EMBL Data Library, July 1995 A;Description: Short form of heparin binding EGF-like growth fac
                                                                                                                                   A; Reference number: S58117
A; Accession: S58117
                                                                                                                                                                                                                                                                                                                               RESULT 11
S58117
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A;Ression: T46914
A;Status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-346 < AAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein DKFZp564L1878.1 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004 C;Accession: T46914
                                                                                                               Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                 294 GYTGOHCEKKDYSVLYVVPGPV-RFQYVLIAAVIGTIQIAVICVVVLCITR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 ILVVSEGSCA-----TDAGSG-----SGDGVHEGSGETSQKETSTCDICQFGAECDEDAE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 LIIIGSGHYAAGLDINDTYSGKREPFSGDHSADGFEVTSRSEMSS-----GSEISPVSE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      EYFGERÇGEKSMKTHSMIDSSLSKIALAAJAAFMSAVILTAVAVITVQLRR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVWCVCNIDCSQTNFNPLCASD---GKSYDNACQIKEASCQKQEKIEVMSLGRCQDNTTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTKSEDGHYARTDYAENANKLEESAREHHIPCPEHYNGFCMHGKCEHSINMQEPSCRCDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SENTSDKPKRKKKGGKNGKNRRNRKKKN--PÇNAEFQNFCIHGECKYIEHLEAVTCKCQQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------MPSSSEPSSGADYDYSEEYDNEPQI--PGYIVDDSVRVEQVVKPPQNKTE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNRGRRQKQ 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRCESGYTGQHC-EKTDFSILYVVPSRQKLTHVLIAAIIGAVQIAIIVAIVMCITRKCPK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CKCQQEYFGERCGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVAVITVQLRRQYVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENTS----DKPKKKKKGGKNGKNRRNR---KKKNPCNAEFONFCIHGECKYIEHLEAVT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYEGEAEER 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYSFNPVCASDGSS----
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                                                                                                                                                                    heparin binding EGF-like growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 143; DB 2; Length 346; Pred. No. 0.0009; 6; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----YNN----PCFVREASCIKQEQIDIRHLGHCTDT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       February 2000
                                                                                                                                                                                                                                                     09-Jul-2004
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                                     PID:g105
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Score 137;

DB 2;

Length 141;

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RESULT 12
A37408
betacellulin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_ch
C;Date: 17-Apr-1993 #sequence_revision 17-Apr
                                 A;Cross-references: DDB:AB001576; NID:g2605478; PIDN:BAA23348.1; PID:g2605479
A;Experimental source: PC-12 cell
C;Comment: This protein is a member of the epidermal growth factor family. It is ating the differentiation of MDA-MB-453 cells.
C;Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homolog C;Keywords: glycoprotein
F;274-327/Domain: Ig-like #status predicted <IGL>
F;361-397/Domain: BGF homology <EGF>
F;462-444/Domain: hydrophobic #status predicted <HYD>
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JC5702
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A;Residues: 1-177 <SHI>
A;Crose-referendes: UNIPROT:Q05928; GB:L08394; NID:g293852; PIDN:AAA40511.1; PID:g293853
C;Keywords: transmembrane protein
F;69-104/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 'F', 212-213, 223-860 <HI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: PC4417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not A;Molecule type: mRNA A;Residues: 1-860 <HIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, J. Biochem. 122, 675-680, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: nucleic acid sequence not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Cross-references: UNIPROT:035569; DDBJ:D89996; NID:g2605631; PIDN:BAA23345.1; ;Experimental source: PC-12 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. 122, 675-680, 1997
[Title: A novel brain-derived member of the epidermal growth factor family that Reference number: JC5700; MUID:98006324; PMID:9348101
;Accession: JC5702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rbB kinase activator alpha2a, brain and thymus - rat
;Species: Rattus norvegicus (Norway rat)
;Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 09-Jul-2004
;Accession: JC5702; PC4417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTHSMIDSSLSKIALAAIAAFMSAVILTAVAVITV--QLRRQYVRKYEGEAEERKK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYIEHLEAVIC 170
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Pred. No. 0.029;
5; Mismatches 5
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2; Mismatches 21;
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   (covalent) #status predicted
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A; Molecule type: mRNA
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A;Reference number: A25531; MUID:87066721; PMID:3491360
A;Accession: A25531
                                      C;Species: Homo sapiens (man)
C;Date: 30-Nov-1980 #sequence revision 14-Aug-1998 #text change
C;Accession: A25531; A01388; A33517; A29721; S45282; S45283
R;Bell, G.I.; Fong, N.M.; Stempien, M.M.; Wormsted, M.A.; Caput,
Nucleic Acids Res. 14, 8427-8446, 1986
A;Title: Human epidermal growth factor precursor: cDNA sequence,
                                                                                                                    epidermal growth factor precursor [validated] N;Alternate names: urogastrone precursor C;Species: Homo sapiens (man) C;Date: 30-Nov-1980 #sequence revision 14-Aug-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Gardner, M.J.; Tettelin, H.; Pertea, M.; Salzberg, S.; Science 282, 1126-1132, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          merozoite surface antigen MSP-4 (EGF domain) PFB0310c - malaria parasite (PC;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, alzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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A; Albas | Reletition | Ag25-Ag25 |
A; Allitrons: 43/1; 109/3; 170/2; 246/2; 314/1; 356/3; 397/1; 438/1; 480/1; 525/3; 575/2; 6
C; Superfamily: epidermal growth factor precursor; EGF homology; LDL receptor YWTD-contail
C; Reywords: duplication; growth factor precursor; EGF homology; LDL receptor YWTD-contail
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-103/Domain: epidermal growth factor proprotein, membrane bound form #status predicted <SIG>
F;43-479/Region: EGF precursor long repeat cLR1>
F;46-85/Domain: LDL receptor YWTD-containing repeat homology <YW01>
F;44-479/Again: LDL receptor YWTD-containing repeat homology <YW02>
F;128-169/Domain: LDL receptor YWTD-containing repeat homology <YW03>
F;170-21/Domain: LDL receptor YWTD-containing repeat homology <YW06>
F;212-256/Domain: LDL receptor YWTD-containing repeat homology <YW06>
F;213-35/Domain: EGF homology <EG1>
F;36-35/Domain: EGF homology <EG3>
F;401-436/Domain: EGF homology <EG3>
F;401-436/Domain: EGF homology <EG3>
F;401-436/Domain: EGF homology <EG3>
F;401-436/Domain: LDL receptor YWTD-containing repeat homology <YW07>
F;524-566/Domain: LDL receptor YWTD-containing repeat homology <YW07>
F;524-566/Domain: LDL receptor YWTD-containing repeat homology <YW07>
F;548-569/Domain: LDL receptor YWTD-containing repeat homology <YW07>
F;548-569/Domain: LDL receptor YWTD-containing repeat homology <YW07>
F;556-594/Domain: LDL receptor YWTD-containing repeat homology <YW07>
F;557-30/Domain: LDL receptor YWTD-containing repeat homology <YW07>
F;558-594/Domain: LDL receptor YWTD-containing repeat homology <YW07>
F;658-737/Domain: LDL receptor YWTD-containing repeat homology <YW01>
F;658-737/Domain: EGF homology <EG3>
F;739-737/Domain: EGF homology <EG3>
F;739-737
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C;Comment: EGF is released in the pancreas, small intestine, mammary gland, and (in some C;Comment: The EGF precursor is found in kidney as a receptor-like membrane-bound proteins.
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Biochem. Biophys. Res. Commun. 145, 126-133, 1987
A;Title: Purification and characterization of high molecular weight human epidermal grow
A;Reference number: A29721; MUID:87241488; PMID:3297054
A;Accession: A29721
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A;Residues: 971-1023 <GRE>
A;Residues: 971-1023 <GRE>
A;Note: some of the molecules lack Arg-1023
R;Furuya, M.; Akashi, S.; Hirayama, K.
Biochem. Biophys. Res. Commun. 163, 1100-1106, 1989
Biochem. Biophys. Res. Commun. 163, 1100-1106, 1989
A;Title: The primary structure of human EGF produced by genetic engineering, studied
A;Reference number: A33517; MUID:89391964; PMID:2789514
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A;Note: intron positions were also determined
R;Gregory, H.; Preston, B.M.
Int. J. Pept. Protein Res. 9, 107-118, 1977
A;Title: The primary structure of human urogastrone.
A;Reference number: A01388; MUID:77117897; PMID:300079
A;Accession: A01388
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A; Residues: 971-1023 < FUR>
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;Residues: 'MKKYP',970-1023 <SV2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene: GDB:EGF
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F;1058-1207/Domain: intracellular #status predicted <INT>
F;31058-1207/Domain: intracellular #status predicted <INT>
F;318-30,325-339,341-354,360-371,367-380,382-395,401-412,408-421,423-436,439-451,447-44-fide bonds: #status predicted
fide bonds: #status predicted
F;976-990,984-1001,1003-1012/Disulfide bonds: #status experimental
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F;916-951/Domain: EGF homology <EG8>
F;971-1023/Product: epidermal growth factor #status
F;976-1012/Domain: EGF homology <EG9>
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  1011 RCQYRDLKWWELRHAGHGQ---
                                                180
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                                                                                                                                                                                                                                                                 876 MGVPVCPPAS---SKCINTEGGYVC--RCSEGYQG----
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                                                                                                                                                                                                                                                                                                        1 MRAPLLPPAPVVLSLLILGSGHYAAGLDLNDTYSGKREPFSGDHSADGFEVTSRSEMSSG
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                                            RCGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVAVITV 221
                                                                                     -----HYSVRNSDSECPLSHDGYCLHDGVCMYIEALDKYACNCVVGYIGE
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ative 22; Mismatches
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Search completed: February 26, 2005, 16:45:00 Job time : 42 secs

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Result
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1: uniprot_sprot:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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 Q06186
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Q8k3e3
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MIM; 104640; ...
GO; GO:0005615; C:extracellular space; TAS.
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GO; GO:0008283; F:cell proliferation; TAS.
GO; GO:0007267; F:cell-cell signaling; TAS.
InterPro; IPR000742; EGF_2.
InterPro; IPR006209; EGF_like.
Pfam; PF00008; EGF; 1.
PROSITE; PS00102; EGF_1;
PROSITE; PS00026; EGF_3; 1.
                                                                                                                                                                                   EMBL; M30704; AAA51791.1;
EMBL; M30702; AAA51773.1;
EMBL; M30698; AAA51773.1; JOINED.
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MEDLINE=93090386; PubMed=1333777;
Culouscou J.-M., Remacle-Bonnet M.,
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SEQUENCE OF 101-184.
SEQUENCE OF 101-184.
MEDLINE=89162036; PubMed=2466334;
Shoyab M., Plowman G.D., McDonald V.L., Bradley J.G., Todaro G.J.;
"Structure and function of human amphiregulin: a member of the epidermal growth factor family.";
Science 243:1074-1076(1989).
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MEDINES-8320474; PubMed=3413110;
Shoyab M., McDonald V.L., Bradley J.G., Todaro G.J.;
"Amphiregulin: a bifunctional growth-modulating glycoprotein produced by the phorbol 12-myristate 13-acetate-treated human breast adenocarcinoma cell line MCF-7.";
Proc. Natl. Acad. Sci. U.S.A. 85:6528-6532(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Bifunctional growth-modulating glycoprotein. Inhibits growth of several human carcinoma cells in culture and stimulates proliferation of human fibroblasts and certain other tumor cells. INDUCTION: By phorbol 12-myristate 13-acetate (pMA). MISCELLANBOUS: AR is a protein containing cysteines in disulfide contain oligosaccharides and/or lipid moieties that are not obligatory for the biological activity. AR may chilagatory for the biological activity. SIMILARITY: Belongs to the amphiregulin family.

SIMILARITY: Contains 1 EGF-like domain.
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PS00022; EGF 1; 1.
PS01186; EGF 2; FALSE_NEG
PS50026; EGF 3; 1.
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Q1-JUN-2001 (TrEMBLrel. 1:
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             Pfam; PF00008; EGF; 1.
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PROSITE; PS00022; EGF 1; UNKNOWN_1.
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EGF-like domain.
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                                                                     InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF like
InterPro; IPR006210; IEGF.
InterPro; IPR006211; IEGF.
Pfam; PF00008; EGF; 1.
SMART; SM00181; EGF; 1.
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Submitted (MAR-2001) to the
-1- SIMILARITY: Contains 1 |
EMBL; AYOZ8310; AAKZ7728 1;
HSSP, Q99075; 1XDT.
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Sus scrofa (Pig).
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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Best Local S
Matches 179
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                                                                                                                                                                                                                                                                                                                                 CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2001) to the EMBL/GenBank/DDBJ

-- SIMILARITY: Contains 1 EGF-like domain.

EMBL; AYO28311; AKC27729.1; -.

HSSP; Q99075; 1XDT.
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01-JUN-2001 (TremBLrel.
01-MAR-2004 (TremBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000742;
InterPro; IPR006209;
InterPro; IPR006210;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amphiregulin short form.
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95
E 216 AA;
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                   SDKPKRKKKGGKNGKNRRNRKKKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQBYFGER
                                                                                                       SEISPVSEMPSSSEPSSGADYDYSEESYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENT
                                                                                                                                                                                                                                                                                                                                                                                          PS00022; EGF_1;
PS50026; EGF_3;
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                                                                                  SEAPPASEMP
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                                                                                                                                                                                                                                                  Conservative
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23571 MW;
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IEGF.
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                                                                                                                                                                                                                                                                 71.9%;
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                                                                                                                                                                                                                                             Score 941; DB Pred. No. 9.3e 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Pred. No. 7.9
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nBank/DDBJ databases.
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ches 18;
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Sus.
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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bond H., Kondo S.,
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bond H., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baidarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,
RA Balla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sultana R., Takenaka Y., Taylor M.S., Setou M., Shimada K.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Wilming L.G., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Pukuda S.,
RA Kanai A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Yasunishi A., Pashizaki Y.;
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Yasunishi A., Hashizaki Y.;
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P31955;
01-JUL-1993
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Amphiregulin precur-
Name=Areg; Synonyms=Sdgf;
Name=Areg; (Mouse).
SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE=Mammary gland;
MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Androgen-responsive expression and mitogenic aderived growth factor on an androgen-dependent carcinoma cell line.";
Biochem, Bionhvo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Cecum; MEDLINE=22354683; PubMed=12466851; DOI=10,1038/nature01266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96174905;
Das S.K., Chakrabo
Dey S.K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Amphiregulin is an implantation-specific and progesterone-regulated gene in the mouse uterus.";
Mol. Endocrinol. 9:691-705(1995).
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Mammalia; Eutheria;
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                                                                                                                                                                "Analysis of
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                                                                                                                             full-length cDNAs
420:563-573 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5174905; PubMed=8592515;
Chakraborty I., Paria B.
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(Rel. 44, Last annotation update)
precursor (AR) (Schwannoma-derived
                                                                                                                                                                the mouse transcriptome
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOI=10.1210/me.9.6.691; .C., Wang X.N., Plowman
                                                                                                                                                                 based
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                                                                                                                                                                 annotation
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ouse mammary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR, JH0612; JH0612

HSSP, Q99075, 1XDT.

MGD; MGI:88068, AREG.

InterPro; IPR000742; EGF 2.

InterPro; IPR006209, EGF 1; 1.

PROSITE; PS000022; EGF 1; 1.

PROSITE; PS01026; EGF 2; FALSE NEG.

PROSITE; PS01026; EGF 3; 1.

Cytokine; EGF 1ike domain; Glycoprote
                                                                                                                                                                                                                                                                   TRANSMEM
DISULFID
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DISULFID
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CARBOHYD
SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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EMBL;
EMBL;
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Similarity
                                                                   REVSTISEMPSGSEI
                                                                        SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENT
                                                                                                                  MRAPLLPPAPVVLSLLIIGSGHYAAGLDLNDTYSGKREPFSGDHSADGFEVTSRSEMSSG
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27
100
135
192
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1165
1065
241
241
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99
248
175
215
215
152
163
104
106
241
27549
                                                                                                                                                                                                              70.2%;
                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                                       Amphiregulin.

EGF-like.

Potential.

By similarity.

By similarity.

By similarity.

N-linked (GLCNAc . . ) (Potential).

N-linked (GlCNAc . . ) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Growth factor; Signal;
                                                                                                                                                                                         Score 918; DB 1;
Pred. No. 6.6e-63;
7; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                             Potential.
                                                                                                                                                                                                                                                        98C61A1B0E75A64E CRC64;
                                                 ŚŚĘŻDNEPO ISGY I IDDSVRVEOVI KPKKNKTEGEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                           41;
                                                                                                                                                                                                                     Length 248;
                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions on
                                                                                                                                                                                     10;
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Q62561;
01-NOV-1996
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SEQUENCE FROM N.A.

MEDIINE-97041064, PubMed-8975671;
Gurskaya N.G., Shagin D.A., Luk'ianov K.A., Va
Shtutman M.S., Musatkin E.A., Moinova E.V., Ta
Luk'ianov S.A., Sverdlov E.D.;

"Cloning cDNA for the ha-SDGF gene from a Syri
with increased metastatic potential using subt
Bioorg, Khim. 22:425-431(1996).

-|- SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00008; EGF; 1
SMART; SM00181; EGF; 1
PROSITE; PS00022; EGF
PROSITE; PS0026; EGF
EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z66535; CAA91439.1;
HSSP; Q99075; IXDT.
InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TYEMPELrel. 01, Created)
01-NOV-1996 (TYEMPELrel. 01, Last sequence update)
01-MAR-2004 (TYEMPELrel. 26, Last annotation update)
Schwannoma derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mesocricetus sp.
                                                                                                                                                                                                                                                                                                             1 MRAPLLPPA-PVVLSLLILGSGHYAAGLDLNDTYSGKREPFSGDHSADGFEVTSRSEMSS
                                                                                                                                   TSDKPKRKKKGGKNGKNRRNRK-KKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQOEYFG
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                            RKKLRQENGNVHAIA
                                                          ERCGEKSMKTHSGDDNDLSKTALAATTVFVSAVTLIAVGIVVIVLLKKRHLKEYEEEAEE
                                                                                     ERCGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVA-VITVOLRRQYVRKYEGEAEE
                                                                                                                                                                                                                                GSEISPVSEMPSSSEPSSGADYDYSEBYDNEBQIPGYIVDDSVRVEQVVKPPQNKTESEN 119
                                                                                                                                                                                                                                                                                   MRTPLLPRALPVLSLLLILGSGHYAAGLDLNGTTSGKSQAPSGHHNATELVV-----SV
                                                                                                                                                                                                          PS00022; EGF_1; UNKNOWN_1.
PS50026; EGF_3; 1.
domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ĊĠĔĸŚĸĸŦĤŚEDĎĸDĹŚĸĨĀVVĀVTIFVŚĀIĨĹĀĀIGIGĪVĨĪVHĹĸĸŖŶFŔĒŶĔĠĔŦĔĔ
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                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           27381 MW; CD920DD40B3D1063 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  67.0%; Score 877; DB 2; 69.4%; Pred. No. 9.6e-60; tive 26; Mismatches 42
248
                                  252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from a Syrian hamster cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    using subtractive hybridization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 AA
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Tatosian A.G.,
                                                                                                                                                                                                                                                                                                                                                                                                       Length
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Best Local Sim
Matches 177;
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DISULFID
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DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 348:257-260(1990).

-I- FUNCTION: Autocrine growth factor as well-range of target cells, among which astro-fibroblasts.

-I- SIMILARITY: Belongs to the amphiregulin contains 1 EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMPR_RAT
P24338;
                                                                                                                                                                                                                                                                                                                                                                             RGD; 2149; Areg.
InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF_like.
Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Eventhe European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitites requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SE MEDLINE=91043095; PubMed=2234093; Kimura H., Fischer W.H., Schubert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992 (Rel.
01-MAR-1992 (Rel.
05-JUL-2004 (Rel.
                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                         Growth
                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01186; EGF 2; FA
PROSITE; PS50026; EGF 3; 1.
Cytokine; Direct protein se
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X55183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amphiregulin precursor (A. Name=Areg; Synonyms=Sdgf;
                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure,
                      121
                                                                                                                                                                                                                                                                                                                                                                                                                              Q99075; 1XDT.
                                                                                                                                                                                                                                                                                                                        factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                          3296; S13296.
                                                                                                                                                  Similarity
                                                                                                    MRAPLLPPAPVVLSLLILGSGHYAAGLDLNDTYSGKREPFSGDHSADGFEVTSRSEMSSG
             SDKPKRKKKGGKNGKNRRNR-KKKNPCNAEFQNFCIHGECKYIEHLEAVTCKCQQEYFGE 179
                                                         SEISPVSEMPSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENT 120
                                                                                        MRTPSLSLALSVLSLLVLGSGHYAAGLELNGTSSGKGEPSSGDHSAGGLVV--
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236
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25
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173
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1161
172
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103
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26633 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 21, Last sequence update)
(Rel. 44, Last annotation update)
precursor (AR) (Schwannoma-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAA38967.1; -.
                                                                                                                                                                                                                                                                                                                       Signal;
KKKGGKGGKGRRNRKKKKNPCAAKFQNFCIHGECRYIENLEVVTCHCHQDYFGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                 66.9%;
                                                                                                                                                                                                                                                                                                                      Transmembrane.
                                                                                                                                                                                                                                                                                                                                   sequencing;
                                                                                                                                                                                                                                                                                                                                                       FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function
                                                                                                                                      24;
                                                                                                                                                                                Amphiregulin.
EGF-like.
Potential.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAC...)
N-linked (GlCNAC...)
N-linked (GlCNAC...)
N-linked (GlCNAC...)
N-linked (GlCNAC...)
N-linked (GlCNAC...)
                                                                                                                                               Score 874.5; DB 1
Pred. No. 1.5e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
3; DOI=10.1038/348257a0;
                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of a
                                                                                                                                                                                                                                                                                                                                  EGF-like domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243
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h astrocytes,
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                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family.
                                                                                                                                     40;
                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth
                                                                                                                                      Indels
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Schwann
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(Potential)
(Potential)
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Best Local Similarity
Matches 120; Conserv
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25-OCT-2004
25-OCT-2004
25-OCT-2004
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
01-MRP-2003 (TrEMBLrel. 23, Last annotation update)
Amphiregulin (Fragment).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae;
       Wang Y., Li J., Leung F.C.;
"Chicken Amphiregulin Gene: cDNA Cloning, Promoter Analysis,
"Chicken Amphiregulin Gene: cDNA Cloning, Promoter Analysis,
Regulation of its mRNA Expression in the Chicken Ovary.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY725336; AAU21467.1; -.
SEQUENCE 210 AA; 23665 MW; B977D786740150CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q645M5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amphiregulin.
Name=AREG;
                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
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165 AA;
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17986 MW;
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; 
; Galliformes; Phasianidae; Phasiani
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annotation update)
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; Cricetinae;
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Best Local Similarity
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SEQUENCE
                                                                                                                                                                                                                                                                                                                      PROSITE; PS00022; EGF 1; UNKNOWN 1.
PROSITE; PS50026; EGF 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Welsh Mountain; TISSUE=Mammary gland;
MEDLINE=9719075; PubMed=9027362; DOI=10.1016/S0303-7207(96)03967-6;
POSTYTH I.A., Taylor J.A., Keable S., Turvey A., Lennard S.;
"Expression of amphiregulin in the sheep mammary gland.";
Mol. Cell. Endocrinol. 126:41-48(1997).
-!- SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF 11ke.
InterPro; IPR006210; IEGF.
Pram; PP00008; EGF; 1.
                                                                                                                                                                                                                                                                                                             EGF-like domain.
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P79199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae, Caprimae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1997 (TrEMBLrel 03, 01-MAY-1997 (TrEMBLrel 03, 01-MAR-2004 (TrEMBLrel 26,
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01-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                     168 VTCKCQQEYFGERCGEK 184
                                                                                                                                                      108 VKPPQNKTESENTSDKPKRKKKGGKNGKNRRNRKKKNPCNABFQNFCIHGECKYIEHLEA 167
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                                                                                  VSCQCYPEYFGERCGEK 77
                                                                                                                                   VKPKKNKTESEKTSDKPKRKKKGGKNGKNRKNRKRKNLCDTEFQNFCIHGKCTFLEQLET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMID-SSLSKIALAAIAAFMSAVILTAVAVITVQLRRQYVRKYEGEAEERKKLRQENGNV 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSSSEPSSGADYDYSEEYDNEPQIPGYIVDDSVRVEQVVKPPQNKTESENTSDKPKRKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PREPÉPAPGSDÝE-EÉBÝEEAPLAHQYLVGDLVRVÉPVVKPKPAKRGSÉKNAGKÉRRKN
                                                                                                                                                                                                                                                                   77
         PRELIMINARY;
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                ΑA;
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                                                                                                                                                                                                                                                               9060 MW;
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                                                                                                                                                                                                                    26.6%;
77.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.3%; Score 435.5; DB 2; 48.6%; Pred. No. 9.1e-26; tive 25; Mismatches 59;
                                                                                                                                                                                                 Score 348; DB
Pred. No. 1.5e-
8; Mismatches
                                                                                                                                                                                                    8;
                                                                                                                                                                                                                                                          00BE7B59AE685F25 CRC64;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
       PRT;
       239
                                                                                                                                                                                          ; DB 2;
1.5e-19;
9;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan R., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan R., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.J., Wagner R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Hownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kizywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Nan Jones S.J. Marra M.A.
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (MAR-2004) to the EMBI
EMBL; BC066705; AAH66705.1; -
InterPro; IPR001336; EGF_1.
InterPro; IPR000742; EGF_2.
InterPro; IPR0006209; EGF_1.
Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                    PROSITE; PRO0009; EGFTGF.

PROSITE; PS01186; EGF 1; 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS50026; EGF 3; 1.

NON_TER 1
                                                                                                                                                                                                                                                                                                                         SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence up
05-JUL-2004 (TrEMBLrel. 27, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOC407664 protein (Fragment).
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                                                                                                                                                                                                                                    45
                                                                                                                                                                                                                                                                             Similarity
                                             ITVOLRROYVRKYEGEAEERKKLROENGNV
                                                                                                   CKYIEHLEAVTCKCQQEYFGERCGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVAV
                                                                                                                                 ----RVAFSTKP--KHPSAMPTTEKTKKRKRKGK-GKGRGN--KKNLCKEBYKDFCIHGV
                                                                                                                                                 DDSVRVEQVVKPPQNKTESENTSDKPKRKKKGGKNGKNRRNKKKNPCNAEFQNFCIHGE
                                                                                                                                                                                                                     SADGFEV----TSRSEMSSGSEISPVSEMPSSSEPSSGADYDYSEEY--DNEPQIPGYIV
                    IAILLALRYHKKDDADVESEEKVKLEATSV
                                                                                CHYQRDLRTHSCY
                                                                                                                                                                                          SLDRFESGKPRTTEVNLLHTSEKTNITGLQADNGTSVGDD-DYEEDYEGDYELNLP----
                                                                                                                                                                                                                                                                                                                         239
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                27024 MW; 49B7FDFDC91925B7 CRC64;
                                                                                                                                                                                                                                                                   17.2%;
32.4%;
                                                                        VCHGGYSGERCHVFTLPVGKEEQRYSRTTALAVIAVVLS---
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                                                                                                                                                                                                                                                          Score 224.5; DB 2
Pred. No. 2.1e-09;
3; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence update)
                                               248
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23;

Gaps

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SMART; SM00181; EGF_1; 1.

PROSITE; PS00022; EGF_2; 1.

PROSITE; PS00186; EGF_3; 1.

PROSITE; PS50026; EGF_3; 1.

PROSITE; PS50026; EGF_3; 1.

PROSITE; PS50026; EGF_3; 1.

PROSITE; PS50026; EGF_3; 1.
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HBGF CERAE
Q09118;
01-FEB-1996
                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s or send an email to license@isb-sib.ch).
  PROSITS; I
EGF-like of
Receptor;
SIGNAL
PROPEP
CHAIN
                                                                                                                                 HSSP; Q99075; 1XDT.
InterPro; IPR000742;
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PIR; A41914; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH FBLN1 MEDLINE=22328967; Pubm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Localization of a critical diphtheria terminus of the mature heparin-binding of the diphtheria toxin receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Naglich J.G., Metherall J.E., Russel D.W., Eidels L., "Expression cloning of a diphtheria toxin receptor: i heparin-binding EGF-like growth factor precursor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=DTR; Synonyms=HBGPL;
Cercopitheous aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Heparin-binding EGF-like growth factor precursor
(Diphteria toxin receptor) (DT-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOXIN-BINDING DOMAIN. MEDLINE=95126975; Pul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 69:1051-1061(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=92/198386; PubMed=1606612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel.
05-JUL-2004 (Rel.
                                                                                                 Pro; IPR006209; E
Pro; IPR006210; I
PF00008; EGF; 1.
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  ignal;
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63
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                                                                                                                                                              -; NOT_ANNOTATED_CDS
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  Transmembrane.
19 Pot.
62 By 1
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                                                                                                            ; EGF_2.
; EGF_like.
; IEGF.
Potential.
By similarity.
Heparin-binding
                                           Growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOI=10.1186/1471-2121-3-2;
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                                            factor;
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                                                                                                                                                                                                                                                                                                             protein. Mature HB-
and probably binds
  EGF-like
                                           Heparin-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth
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  growth factor
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Best Loc
Matches
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Kimmerly W., Bouce
Kimmerly W., Bouce
Kadner K., Miguel T., Mille
Kadner K., Martin C.F
Subramanian S., Martin C.F
Subramanited (APR-1998) to t)
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TRANSMEM
DOMAIN
DOMAIN
CARBOHYD
CARBOHYD
DISULFID
DISULFID
DISULFID
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W., Rieder M.J., Livingston R.J., Nguyen D.A., Poel C.L., Robertson P.D., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;

SCHACKWITZ W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;

"NIEHS-SNPB, environmental genome project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";

Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heparin-binding EGF-like growth factor precursor (Diphteria toxin receptor) (DT-R).
Name=DTR; Synonyms=HEGFL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel.
01-JUN-1994 (Rel.
25-OCT-2004 (Rel.
                                                                                                         TISSUE=Eye
                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Higashiyama S., Abraham J.
"A heparin-binding growth
that is related to EGF.";
Science 251:936-939(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Macrophage;
MEDLINE=91157008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=1840698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
160
184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Pred.
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O-linked
O-linked
O-linked
By simila:
By simila:
By simila:
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Cytoplasmic (Po
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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similarity.
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No. 1.7
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nes 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fiddes J.C., Klagsbrun M.;
d by macrophage-like cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Potential)
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similarity).
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Rojeski
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                     G.D.,
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A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Hilling M., Madan A., Touchman J.W., Green E.D., Dickson M.C., A Butterfield Y.S.N., Touchman J.W., Green E.D., Dickson M.C., A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., "Generation and initial analysis of more than 15,000 full-length humar rei" Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
             EMBL; M60278; AAA35956.1; -.
EMBL; AC004634; AAC15470.1; -.
EMBL; AC003097; AAH33097.1; -.
EMBL; AY164533; AAA46738.1; -.
PIR; A38432; A38432.
PDB; 1XDT; X-ray; R=69-147.
Genew; HGNC:3059; DTR.
H-INCDB; HIX0005230; -.
                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                           entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 73-147 IN COMPLEX WITH TOX. MEDILINE=98324089, PubMed=9659904; DOI=10.1016/S1097-2765(00)80008-8; Louie G.V., Yang W., Bowman M.E., Choe S.; "Crystal structure of the complex of diphtheria toxin with an extracellular fragment of its receptor."; Mol. Cell 1:67-78(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE-95138082; PubMed=7836353; DOI=10.1074/jbc.270.3.1015; Mitamura T., Higashiyama S., Taniguchi N., Klagsbrun M., Mekada E. "Diphtheria toxin binds to the epidermal growth factor (EGF)-like domain of human heparin-binding EGF-like growth factor/diphtheria toxin receptor and inhibits specifically its mitogenic activity."; J. Biol. Chem. 270:1015-1019(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 63-141 AND 143-148, AND CARBOHYDRATE-LINKAGE SITES.
TISSUE-Histiocytic lymphoma;
TISSUE-Histiocytic lymphoma;
MEDLINE-92210596; PubMed=1556128;
Higashiyama.S., Lau K., Besner G.E., Abraham J.A., Klagsbrun M.
"Structure of heparin-binding EGF-like growth factor. Multiple
primary structure, and glycosylation of the mature protein.";
J. Biol. Chem. 267:6205-6212(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOXIN-BINDING DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: May be involved in macrophage-mediated cellular proliferation. It is mitogenic for fibroblasts and smooth but not endothelial cells. It is able to bind EGF receptor higher affinity than EGF itself and is a far more potent m for smooth muscle cells than EGF.

SUBCELLULAR LOCATION: Type I membrane protein. Mature HB-I released into the extracellular space and probably binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor.
PTM: Seve
                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                    to be biologically active.

PTM: O-linked glycan attachment sites wer
degradation, O-glycanase digest suggests
(done in HB-EGF purified from histiocytic
VDB; HIX0005230;
126150; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Several N-termini have been identified by diforms with N-termini 63, 73 and 74 have been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                             digest suggests m
                                                                                                                                                                                                                                                                                                                                                                                     domain.
                                                                                                                                                                                                                                                                                                                                                                                                                        were determined by Edman sts mucin-type glycosylation ytic lymphoma cell line U-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tein. Mature HB-EGF probably binds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             direct sequencing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptors
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Scheetz T.E.,
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SOCOR BITTORI
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Best Local S
Matches 55
                                                             HBGF PIG
Q01580;
01-FEB-1996
30-MAY-2000
05-JUL-2004
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartiod;
NCBI_TaxID=9823;
                                                 01-FEB-1996 (Rel. 33, Created)
30-MAY-2000 (Rel. 39, Last sequence upo
5-UUL-2004 (Rel. 44, Last annotation upo
Heparin-binding EGF-like growth factor
                                                                                                                                                                                                                                                                                                                        TURN
STRAND
SEQUENCE
                               Name=DTR; Synonyms=HEGFL;
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
TURN
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CARBOHYD
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DOMAIN
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TRANSMEM
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GO; GO:0005817; C:integral to plasma membrane; TAS.
GO; GO:000514; P:epidermal growth factor receptor binding; TAS.
GO; GO:0007517; P:muscle development; TAS.
GO; GO:0008204; P:positive regulation of cell proliferation; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3D-structure; Direct Glycoprotein; Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00022; EGF 1;
PROSITE; PS01186; EGF 2;
PROSITE; PS50026; EGF 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROPEP
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                                                                                                                                                           179
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                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                        VGLLMFRYHRRGGYDVENEEKVKLGMTNSH
                                                                                                                                                                                                 KYVKELRAPSCI
                                                                                                                                                                                                                 KYIEHLEAVTCKCQQEYFGERCGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVAVI
                                                                                                                                                                                                                                                         DSVRVEQVVKPPQNKTESENTSDKPKRKKKGGKNGKNRKNRKKKNPCNAEFQNFCIHGEC
                                                                                                                                                                          TVQLRRQYVRK--YEGEAEERKKLRQENGN
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                                                                                                                                                                                                                                                                                 Conservative
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116
134
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                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                               Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                         23067 MW;
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                                                                                                                                                                                               CHPGYHGERCHGLSLPVENRLYTYDHTTILAVVAVVLSSVCL---LVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein factor;
                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Or 72, or 73, or 76, or 81.

Heparin-binding EGF-like grc C-terminal (Potential).

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

EGF-like.

By similarity.

By similarity.

By similarity.

By similarity.

O-linked (GalNAc. . .).

O-linked (GalNAc. . .).
                                                                                                                                                                                                                                                                              Score 211.5; DB
Pred. No. 1.7e-08
3; Mismatches 5
         Craniata; Vertebrata;
actyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing; EGF-like domain;
Heparin-binding; Receptor; S
                                                                                                                                                                                                                                                                                                                       2C43C9D1D8291B51 CRC64;
                                                                       update)
                                                 n update)
or precursor
                                                                                                     208
                                                                                                                                                                            247
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                                                   (HB-EGF)
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Sus.
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                                                  (HBEGF)
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Best Local S
Matches 62
                                                                                                                                                                   DISULFID
DISULFID
                                                                                                                                           CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              Pfam; PFO PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y15731; CAA75740.1;
EMBL; X67295; CAA47709.1;
PIR; S27162; S27162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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"Tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93075016; PubMed=1445231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pascall J.C.;
Submitted (NOV-1997)
                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000742; EGF_2.
InterPro; IPR006209; EGF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                   PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gland.
- PTM: O-glycos
- SIMILARITY: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: May be involved in macrophage-mediated cellular proliferation. It is mitogenic for fibroblasts and smooth muscle but not endothelial cells. It is able to bind EGF receptors with higher affinity than EGF itself and is a far more potent mitogen for smooth muscle cells than EGF (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein. Mature HB-EGF is released into the extracellular space and probably binds to a receptor (By similarity).

TISSUE SPECIFICITY: Macrophages, midbrain, cerebellum, hypothalamus, cerebral cortex, bulbourethral gland, lung, heart receptors.
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levels in lymph node, thymus, spleen;
olfactory bulb, thyroid, duodenum, par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                 110
                                                                                                                                                                                                                                                                                                                                                                            PF00008; EGF;
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                                       30
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                                                                                          62; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O-glycosylated (
LARITY: Contains
PPQNKTESENTSDKPKRKKKGGKNGKNRRNRKKKNPCNABFQNFCIHGECKYIEHLEAVT
                                                                                                                                                                                                                                                                                                                                      PS50026;
                                         RRGLADGTSNLVSPTESTDQLLPPGGGRGREVLDLEEADL
                                                                                                                                                                                                                                                                                                                       domain;
                                                                 RSEMSSGSE--ISPVSEMPSSSEPSSGADYDY--SEEYDNEPQIPGYIVDDSVRVEQVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      white;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pascall J.C., E
                                                                                                                                      23
148
208
161
161
142
144
144
143
143
143
143
22986
                                                                                                                                                                                                                                                                                                                       Glycoprotein;
                                                                                                                                                                                                                                                                                                                                   EGF_1; 1.
EGF_2; 1.
EGF_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Heart;
                                                                                                     15.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ូ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EGF-like domain.
                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                        ! :
                                                                                          30;
                                                                                                                                                   Potential.

Cytoplasmic (Potential).

EGF-like.

By similarity.

By similarity.

By similarity.

By similarity.

C-linked (GalNAc...) (B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brown
A for h
                                                                                       Score 208.5; DB
Pred. No. 3e-08;
0; Mismatches
                                                                                                                                                                                                                                                                                Potential.
By similar
                                                                                                                                                                                                                                           Heparin-binding EGF-like g C-terminal (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                       Growth
                                                                                                                                           0A7DA97AE30C8967
                                                                                                                                                                                                                                                                                  similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n K.D.;
heparin-binding
                                                                                                                                                                                                                                                                                                                      factor; Heparin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bourethral gland, lung, heart seminal vesicle, testis; at leart, not detected in pituitary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pancreas, liver, submaxillary
                                                                                                              DB 1;
                                                                                          75;
                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epidermal
                                                                                          Indels
                                                                                                                 Length
                                                                                                                                                     (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
                                                                                                                                                                                                                                                                    growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                  208;
                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth
                                         DLLRADFSSK
                                                                                                                                                                                                                                                                    factor
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                                                                                                                                          Matches
                                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=breed White Leghorn;

MEDLINE=99254107; PubMed=10318950; DOI=10.1073/pnas.96.10.5716;

Pu S.l., Bottoli I., Goller M., Vogt P.K.;

"Heparin-binding epidermal growth factor-like growth factor, a target gene, induces oncogenic transformation.";

Proc. Natl. Acad. Sci. U.S.A. 96:5716-5721(1999).
                                                                                                                                                                                                  PROSITE;
PROSITE;
PROSITE;
EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9W7C5
Q9W7C5;
                                                                                                                                                                                                                                              Pfam; PF00008; EGF; SMART; SM00181; EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                           Fu S.L., Bottoli I., Goller M., V
Submitted (FEB-1999) to the EMBL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999
01-MAR-2004
                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                    InterPro; IPR000742;
InterPro; IPR006209;
InterPro; IPR006210;
                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 EMBL; AF131224; AAD29416.1;
                                                                                                                                                                                                                                                                                                                                                                 STRAIN=breed White Leghorn;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=HB-EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heparin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999
                                                                                                                                                                                                                                                                                                        HSSP; Q99075; 1XDT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
181
                        212
                                               121
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                                                                                           69
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                                                                                                                                          50;
                                                                                                                                                                                                        ; PS00022; EGF_1;
; PS01186; EGF_2;
; PS50026; EGF_3;
                                                                                                                                                     Similarity
                       ILTAVAVITVQLRRQYVRKYEGEAEERKKL
                                                                     IHGECKYIEHLEAVTCKCQQEYFGERCGEKSMKTH---
                                                                                                                GYIVDDSVRVEQVVKPPQNKTESENTSDKPKRKKKGGKNGKNRRNRKKKNPCNAEFQNFC
                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGGYDVENEEKVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K--YEGEAEERKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQALATPSK--EERGKRKKKGKGLG-----KKRDPCLRKYKDFCIHGECKYVKELRAPS
                                                                                          GDALSELPRVAFLSKPQGPVT-----PKKKGNGNKRRKGKGLGKKRDPCLRKYKDFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CICHPGYHGERCHGLSLPVKNRLYTYDHTTILAVVAVVLSSVCL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKCQQEYFGERCGEKSMKTHSMIDSSLSKIALAAIAAFMSAVILTAVAVITVQLRRQYVR
                                                                                                                                                                                    212 AA; 22541 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 26, Last snotation updat
ding EGF-like growth factor.
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            White Leghorn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                               EGF;
                                                                                                                                                                                                                                                           ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi;
Weognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                      IEGF.
                                                                                                                                                     33.3%;
                                                                                                                                                              15.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
                                                                                                                                                                                                                                  UNKNOWN_1.
 -GVYDVENBEKIKL
                                               COPGYHGERCHGLLLPVEHPPSTYDHTTALAVVAVVLSSLCLV
                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                EGF-like
                                                                                                                                                   Score 198.5;
Pred. No. 1.8
                                                                                                                                                                                      E82A8D08F5297183 CRC64;
                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                           Vogt P.K.;
//GenBank/DDBJ
                                                                                                                                                     No. 1.8e-07;
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                        241
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                                                                                                                                                                DB
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                                                                                                                                          13
                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                            databases.
                                                                    SMIDSSLSKIALAAIAAFMSAV
                                                                                                                                          Indels
                                                                                                                                                             Length
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                                                                                                                                          15;
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                                               180
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RESULT 15 Q9BG62 ID Q9BG6 AC Q9BG6

Q9BG62; Q9BG62;

PRELIMINARY;

PRT;

132

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A Klonisch T., Wolf P., Hombach-Klonisch S., Vogt S., Kuechenhoff A.,

A Tetens F., Fischer B.;

L Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

C -- SIMILARITY: Contains 1 EGF-like domain.

DR EMBL; AR333182; ARK14375.1; -.

DR InterPro; IPR001336; EGF 1.

DR InterPro; IPR001336; EGF 2.

DR InterPro; IPR006209; EGF-1ike.

DR InterPro; IPR006210; IEGF-1.

DR Fam; PF00008; EGF; 1.
                                                                                                                                                                          Query Match 14.9%; Score 195; DB 2; Length 132; Best Local Similarity 34.9%; Pred. No. 1.8e-07; Matches 44; Conservative 22; Mismatches 52; Indels
                                                                                                                                                                                                                                                                     PRINTS, PRO0009, EGFTGF.

SMART; SM00181; EGF; 1.

PROSITE; PS00022; EGF 1; UNKNOWN_1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS50026; EGF 3; 1.

PROSITE; PS50026; EGF 3; 1.
                                                                                                                                                                                                                                             NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Heparin-binding epidermal growth factor (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9986;
                                               127 VCLLVI 132
                             211 VIĻTAV 216
                                                                                                           91 PQIPGYIVDDSVRVEQVVKPPQNKTESENTSDKPKRKKKGGKNGKNRNRKKKNPCNAEF 150
                                                                                                                                                                                                                                      132 132
132 AA; 14628 MW; 6F5ACC07E6A0FF4E CRC64;
                                                                                                                                                                           8
                                                                                                                                                                          Gaps
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Search completed: February 26, 2005, 16:44:14 Job time : 176 secs